*****	(TM)
******	'
******	·======= Î Î

*****	 <u> </u>
******	>>}

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

Mon Mar 8 23:35:29 1999; MasPar time 72.58 Seconds 879.119 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-206-040-1 (1-469) from US09206040A.seq 465 Perfect Score: N.A. Sequence: Comp: Description: Title:

1 ttaacttgcagcgnccaggt.......gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.......ctactatgtaacttctanna

TABLE jmetric Gap 60 Scoring table:

Dbase 0; Query 0 STD : Nmatch 188442 seqs, 68026449 bases x 2 Searched:

Minimum Match O% Listing first 45 summaries Post-processing:

n-geneseq32 Database:

| jpart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part119 18:part18 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 45:part35 36:part36 37:part37 38:part38 39:part40

Variance 2.661; scale 2.659 Mean 7.077; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description Pred. No. Score Match Length DB ID Description Description Description 1 28 6.0 37 791275 CDNA encoding a novel 1.36e-09 2 8 6.0 969 38 796721 Human synaptogyrin cD 1.36e-09 3 28 6.0 1581 22 732233 Cuphea Cl4:0-ACP thio 1.36e-09 4 28 6.0 1588 40 V17199 Human MKK3:interactin 1.36e-09 5 21 4.5 1257 24 738266 54 gene differential 1.09e-03 6 21 4.5 2055 24 738266 54 gene differential 1.09e-03 7 18 3.9 787 21 738208 Primer SALADTT contg. 2.20e-01 9 18 3.9 787 21 729009 Parietaria allergen P 2.20e-01 9 18 3.9 1930 40 V16738 CDNA encoding human C 2.20e-01 C 12 18 3.9 2721 2 010543 BamHI J-I fragment ca 2.20e-01 C 13 18 3.9 2721 2 010543 BamHI J-I fragment ca 2.20e-01 C 2.20e-01 C 13 18 3.9 2721 2 010512 BamHI J-I fragment ca 2.20e-01 C 2.20e-01 C 13 18 3.9 2721 2 010512 BamHI J-I fragment ca 2.20e-01 C 2.20e-0								
Score Match Length DB ID Description 28 6.0 570 37 191275 CDNA encoding a novel 28 6.0 1581 22 132233 CUBhea C14:0-ACP thio 28 6.0 1581 22 132233 CUBhea C14:0-ACP thio 21 4.5 1257 24 138266 54 gene differentiall 21 4.5 2055 24 138266 54 gene differentiall 21 3.9 787 1729008 Parietaria allergen P 22 18 3.9 1930 40 V16738 CDNA encoding human C 23 1930 18 115610 CRCC-1 CDNA encodes C 24 18 3.9 2721 2 2010143 Bamili J-I fragment ca 25 26 2721 2 201212 Bamili J-I fragment ca	Poen1+		8					
570 37 191275 CDNA encoding a novel 1581 22 13223 Human synaptogyrin cD 1581 22 13223 Cuphea Cl4:0-ACP thio 1698 40 V17199 Human WKR3-interactin 1257 24 138266 54 gene differentiall 2055 24 138260 10 gene differentiall 36 13 079345 Primer SALADT Contg. 787 21 129009 Parietaria allergen P 1930 40 V16738 CDNA encoding human C 1930 18 115610 CROC-1 CDNA encodes c 2721 2 010543 BamHI J-I fragment ca 2721 2 010212 BamHI J-I fragment ca	NO.	Score	Match	Length	DB		Description	Pred. No
969 38 T96721 Human synaptogyrin cD 1581 22 T3223 Cuphea C14:0 ACP thio 1589 40 V17199 Human WKK3-interactin 1257 24 T38266 54 gene differentiall 2055 24 T38260 10 gene differentiall 36 13 Q79345 Primer SALADT contg. 787 21 T29008 Parietaria allergen P 845 21 T29009 Parietaria allergen P 1930 40 V16738 CDNA encoding human C 1930 18 T15610 CROC-1 CDNA encodes C 2721 2 Q10243 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca	-	28	6.0	570	37	T91275	cDNA encoding a novel	1.36e-09
1581 22 T32233 Cuphea C14:0-ĀCP thio 1 1698 40 V17199 Human MKR3-interactin 1 2055 24 T38266 54 gene differential 1 2055 24 T38260 10 gene differential 1 36 13 Q79345 Primer SALADIT contg. 2 787 21 T29008 Parietaria allergen P 2 845 21 T29009 Parietaria allergen P 2 1930 40 V16738 CDNA encoding human C 2 1930 18 T15610 CROC-1 CDNA encodes C 2 2721 2 Q10212 BamHI J-1 fragment ca 2 2721 2 Q10212 BamHI J-1 fragment ca 2 2721 2 Q10212	7	28	9.0	696	38	T96721	Human synaptogyrin cD	1.36e-09
1698 40 V17199 Human MKR3-interactin 1 1257 24 T38266 54 gene differential 1 2055 24 T38266 10 gene differential 1 36 13 Q79345 Primer SALADTT contg. 2 787 21 T29008 Parietaria allergen P 2 845 21 T29009 Parietaria allergen P 2 1930 40 V16738 CDNA encoding human C 2 1930 18 T15610 CROC-1 CDNA encodes C 2 2721 2 Q10212 BamHI J-1 fragment ca 2 2721 2 Q10212 BamHI J-1 fragment ca 2 273 2 Q10212	٣	28	6.0	1581	22	T32233	Cuphea C14:0-ACP thio	1.36e-09
1257 24 T38266 54 gene differentiall 1 2055 24 T38260 10 gene differentiall 1 3 679345 Primer SALADTY contg. 2 77 21 T29008 Parietaria allergen P 2 845 21 T29009 Parietaria allergen P 2 1930 40 V16738 CDNA encoding human C 2 1930 18 T15610 CROC.1 CDNA encodes C 2 2721 2 Q10212 BamHI J-1 fragment Ca 2 2721 2 Q10212 BamHI J-1 fragment ca 2 2721 2 Q10212	4	28	6.0	1698	40	V17199	Human MKK3-interactin	1.36e-09
2055 24 T38260 10 gene differentiall 1 36 13 Q79345 Primer SALADTT contg. 2 787 1 T29008 Parietaria allergen P 2 845 21 T29009 Parietaria allergen P 2 1930 40 V16738 CDNA encoding human C 2 1930 18 T15610 CROC-1 CDNA encodes C 2 2721 2 Q10212 BamHI J-1 fragment ca 2 2721 2 Q10212 BamHI J-1 fragment ca 2 2721 2 Q10212	S	21	4.5	1257	74	T38266	54 qene differentiall	1.09e-03
36 13 Q79345 Primer SALADIT contg. 787 21 T29008 Parietaria allergen P 845 21 T29009 Parietaria allergen P 1930 40 V16738 CDNA encoding human C 1930 18 T15610 CROC-1 CDNA encodes c 2721 2 Q10543 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca	9	21	4.5	2055	77	T38260	10 gene differentiall	1.09e-03
787 21 T29008 Parietaria allergen P 845 21 T29009 Parietaria allergen P 1930 40 V16738 CDNA encoding human C 1930 18 T15610 CROC-1 cDNA encodes c 2721 2 Q10543 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca	7	18	9.8	36	13	079345	Primer SALADIT contq.	2.20e-01
845 21 T29009 Parietaria allergen P 1930 40 V16738 CDNA encoding human C 1930 18 T15610 CROC-1 CDNA encodes c 2721 2 Q10543 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca	ထ	18	3.9	787	21	T29008	Parietaria allergen P	2.20e-01
1930 40 V16738 CDNA encoding human C 1930 18 T15610 CROC-1 CDNA encodes c 2721 2 Q10543 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca	σ	18	3.9	845	21	T29009	Parietaria allergen P	2.20e-01
1930 18 T15610 CROC-1 CDNA encodes c 2721 2 Q10543 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca	10	18	ه. ه.	1930	40	V16738	cDNA encoding human C	2.20e-01
2721 2 Q10543 BamHI J-I fragment ca 2721 2 Q10212 BamHI J-I fragment ca 3	11	18	3.9	1930	18	T15610	CROC-1 cDNA encodes c	2.20e-01
2721 2 Q10212 BamHI J-I fragment ca	c 12	18	9.8	2721	~	Q10543	BamHI J-I fragment ca	2.20e-01
	c 13	18	ω 9.	2721	~	010212	BamHI J-I fragment ca	2.20e-01

	Ξ:	•	٠	1.17e+00	1.17e+00	1.17e+00	7	17	1.17e+00	17e+	1.17c/06	_	1.17e+00	1.17e-00	.17	1.17e + 00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	1.17e+00	7et	5.896-00
	_	י מאוואר	Human clone 34 gene.	encoding h	CROC-4 cDNA encodes c	Human NDF-alpha3 clon	Rat epithelial membra	4	Interferon gamma indu	gamma	0	Human NDF-alpha2b clo	a	c		Mouse neurotactin cDN	Human NDF-alpha2b clo	Porcine growth hormon	Novel human gene, des	1-1 q	P. falciparum EBL-el	Rat NDF clone 20 DNA.	P. falciparum E31a ge	la ger	200 gene differential	Rat NDF clone 41 DNA.	Rat NDF clone 19 DNA.	Murine short form Ob	Cell membrane proton-		rn vector	cDNA encoding human C
	മെ	n 1	88	V16740	T15611	080219	T85935	322	T74988	T74987	080230	080218	T99584	096100	T39792	T93211	980217	T47497	T95700	T72894	083526	080227	083527	8	T38265	080231	22	T69590	V02308	959	S	V16740
	36	31	32	40	18	13	35	13	34	34	13	13	40	16	35	38	13	56	37	32	14	13	14	32	24	13	13	31	38	31	36	40
	7 2 2 2 2	1	543	925	925	946	1003	1098	1101	1101	1261	1651	1665	1700	1734	1784	1807	1983	2232	2288	2288	2531	2606	2606	2712	2743	2914	3097	3451	3854	5030	925
	w	٠	٠	3.7	•	•	•	3.7	•					•			•	•	•		3.7	•		•		•	3.7		3.7	3.7	3.7	3.4
	17	1	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	16
,	4 5	1	16	17	18	19	20	21	22	23	24	52	56	27	78	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45
											υ						ပ					υ				O	ပ					ပ

ALIGNMENTS

RESULT

The present DNA sequence encodes a novel beta-chemokine polypeptide designated PTEC. The protein has Cys residues of a beta-chemokine (C32, C33, C55 and C72). The present sequence was isolated from a cDNA library generated from non-tumourous human prostate tissue. The PTEC protein is a homologue of human RANTES, which is a C-C chemokine with structural similarity to interleukin-8 and human MIP-lbeta. The polynucleotide sequence encoding PTEC can be used to diagnose or treat a condition associated with the presence of activated T cells including viral, bacterial, fungal or helminthic infections, allergic or asthmatic responses, mechanical injury associated with trauma, arteriosclerosis, atherogenesis or collagen vascular diseases, autoimmune diseases such as rheumatoid arthritis, myasthenia gravis, systemic lupus erythematosus or haemolytic anaemla, leukaemla, lymphomas or carcinomas, and diseases of PTEC, a novel human beta-chemokine - useful for diagnosing and treating e.g. viral, bacterial, fungal infections, auto-immune diseases, etc claim 2; Pages 39-40; 59pp; English. 23.4APR-1998 (first entry)
CDNA encoding a novel beta-chemokine designated PTEC.
Beta-chemokine; PTEC; homologue; human RANTES; C-C chemokine;
dlagnosis; treatment; activated T cell;
immediate type hypersensitivity; leukocyte proliferation; ss. Location/Qualifiers 110..391 /*tag= a 23-OCT-1997. 14-APR-1997; UO6249. 17-APR-1996; US-633682. (INCY-) INCYTE PHARM INC. Bandman O. Hawkins PR, Murry LE; PPSDB; W27271. ВР. r 1 T91275 standard; cDNA; 570 WO9739126-A1. Homo sapiens Key

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            а
                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polynucleotide (snpg) identifies and encodes a novel human This polynucleotide (snpg) identifies and encodes a novel human Synaptogytin homologue (SNPG) (see W36516). It was initially identified in Incyte Clone 775126 from a colon cDNA library (COLNNOTOS) prepared from a Crohn's disease patient. Also claimed are: (1) an expression vector containing PN; (2) a host cell transformed with the vector of (1); (3) the purified 224 amino acid SNPG protein; (4) an antisense molecule complementary to PN; (5) an inhibitor specific for the polypeptide of (3); and (6) an inhibitor specific for the polypeptide of (3); and (6) an inhibitor specific for the polypeptide of (3); and (5) and cancers or tumours of the lung, colon or brain (claimed). The antisense molecule, Ab or inhibitor can be used to treat, e.g. The antisense molecule, Ab or inhibitor can be used to treat, e.g. Sequence 969 BP; 163 A; 324 C; 280 G; 202 T;
                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
  excessive
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                    Human synaptogyrin cDNA.'
Synaptogyrin, human; colon cancer; lung cancer; brain tumour;
Crohn's disease; rheumatoid arthritis; AIDS; allergy; urticaria;
juvenile diabetes; scleroderma; antisense; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human synaptogyrin homologue - useful for diagnosis and treatment of, e.g. rheumatoid arthritis, Crohn's disease, cancers,
immediate type hypersensitivity which involve activation or exces proliferation of leukocytes, particularly monocytes, macrophages, eosinophils, basophil, mast and T cells. 138 G; 128 T; sequence 570 BP; 149 A; 155 C;
                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-OCT-1996 (first entry)
Cuphea C14:0-ACP thioesterase CDNA clone MCT34 (CpFatB2).
Myristate: myristic acid; fatty acid; acyl-ACP thioesterase;
seed oil: oilseed; vegetable oil: Brassica; transgenic plant;
surfactant; ss.
                                                              / Match 6.0%; Score 28; DB 37; Length 570; Local Similarity 100.0%; Pred. No. 1.36e-09; nes 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 38; Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 38; I
Pred. No. 1.36e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                  59 ggaattcccgggtcgacccacgcgtccg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
110..784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggaattcccgggtcgacccacgcgtccg
                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
Hawkins PR, Murry LE, Stuart SG;
WPI; 97-549677/50.
P-PSDB; W36516.
                                                                                                                                T32233 standard; cDNA; 1581 BP. T32233;
                                                                                                                                                                                   T 2
T96721 standard; cDNA; 969 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                     27-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                             /*tag= a
                                                                                                                                                                                                                                                                                                                                                            00-NOV-1997.
30-APR-1997; U07378.
30-APR-1996; US-700637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cuphea palustris.
Key
                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           W09741143-A1.
                                                                                                                                                                                                                                                                                                                                                        06-NOV-1997
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
ID T3
AC T3
DT 26
DT 26
DE CU
KW MY
KW SU
OS CU
FH KE
                                                                                                                                                                                88888
                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
malignant conditions - comprises nucleic acid, antibodies, fusion proteins and peptide fragments
Disclosure; Page 14; 17pp; English.

This cona and peptide fragments
Disclosure; Page 14; 17pp; English.

This cona encodes a human MKK3 interacting protein (MIP). The mitogenactivated protein kinase (MAPK) kinase-3 (MKK3) is a protein kinase that phosphorylates p38 MAP kinase specifically and is involved in transducing stress signals. The MIP binds to and interacts with a dominant interfering mutant form of MKK3 and may be involved in transducing extracellular signals to the nucleus, resulting in activation of p38 kinase. MIP is expressed in human brain, kidney, liver, lung, pancreas and spleen but not in heart or striated muscle. Detection of MIP in a body sample (particularly a tumour or metastasis) is used to identify the tissue solected from the group consisting of brain, kidney, liver, lung, pancreas or spleen tissue. Fusion proteins comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                           Recombinant prodn. of myristate in plant cells - using DNA with preferential activity on C14 fatty acids from Cuphea palustris, nutmeng and camphor, useful in detergent and food industries Example 1; F19 IA-IE; 77pp: English.
A CDNA clone (732233), designated MCT34 (pCpFatB2), codes for Cuphea palustris C14:0-ACP thioesterase (W02081), an enzyme that acts primarily on C14:0-ACP substrates, forming C14:0 (myristate). It was isolated from a developing seed CDNA library by screening with sequences encoding medium-chain acy1-ACP thioesterases from Cuphea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hookeriana. Constructs for expression of clone MCT34 in plant scads under the control of napin or oleosin regulatory regions were prepd. These allow high-level prodn. of myristate (useful in surfactants and foods) in plant cells, e.g. Brassica. 8equence 1581 BP; 418 A; 356 C; 410 G; 397 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MKK3-interacting protein (MIP) encoding cDNA.
MKK3-interacting protein; MIP; mitogen activated protein kinase;
MAPK kinase-3; human; transduction; target; extracellular signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MKK3-interacting protein, used to identify human tissues in malignant conditions - comprises nucleic acid, antibodies, fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 22; Length 1581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Db 4..,
No. 1.36e-09;
.-haq 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "MKK3-interacting protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ggaattcccgggtcgacccacgcgtccg 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                       01-FEE-1996, U01585,
02-FEB-1995, US-383756,
02-TUN-1995, US-460898,
(CALJ) OLAGENE INC.
Dehesh K, Hawkins D, Voelker TA;
WPI: 96-771439/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V17199 standard; cDNA; 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-1998 (first entry)
119..1354
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167..1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kavanaugh MW, Shyamala V;
WPI; 98-086965/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-1998.
02-JUL-1997; U10866.
01-JUL-1997; US-886572.
03-JUL-1996; US-021224.
12-JUL-1996; US-021641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interfering mutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W52169
                                                                                                                                                                                                                                                                                                                               WPI; 96-371439
P-PSDB; W02081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9800539-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1998
```

/*tag= b /note= "band 10 nucleotide sequence"

Location/Qualifiers 496..1509

/*tag= a 1106..1392

88888888

셤 ò

```
Probable Woulde.

The probable woulder products differentially expressed in Thelper cells are dense and their products differentially expressed in Thelper cells are useful in diagnosis and treatment of immune disorders, e.g. multiple sclerosis, asthma, lepromatous leprosy, etc.

The claim if Fig 9: 218pp; English, 16, 161, 200 and 54 (738260-66)

Novel murine genes 10, 57, 106, 161, 200 and 54 (738260-66)

Novel murine genes 10, 57, 106, 161, 200 and 54 (738260-66)

Mover identified in transgenic T-cell paradigm and T-cell clone paradigm searches for genes which are differentially expressed within and/or among helper T (TH) cell subpopulations. The product (W01046) of the 10 gene (738260) is a receptor protein possibly involved in signal transduction. Gene 10 expression is up-regulated in stimulated TH1 and TH2 cells. The gene is located on the mouse chromosome 12. The gene and its product can be used to reduce the level of induced T-cell activity and bring about the amelioration of a wide range of T-cell related disorders.

Squence 2055 BP; 623 A; 461 C; 414 G; 557 T;
  138260;
29-DEC-1996 (first entry)
10 gene differentially expressed in T helper cells.
T helper cell: TH cell: T-cell: T-lymphocyte: 10 gene; differential expression; immune disorder; multiple sclerosis; asthma; lepromatous leprosy; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                           03-MAR-1995; US-398633.
07-JUN-1995; US-487748.
(MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                 12-SEP-1996.
01-MAR-1996; U02798.
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 96-433404/43.
P-PSDB; W01046.
                                                                                                                                                                                                                                                                             WO9627603-A1.
                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                          Levinson DA;
                                                                                                                                 Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                          g
                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes and their products differentially expressed in T helper cells

" useful in diagnosis and treatment of immune disorders, e.g.

" multiple sclerosis, asthma, lepromatous leprosy, etc.

" claim 1; Fig 22; 218pp: English.

" Claim 1; Fig 22; 218pp: English.

Novel murine genes 10, 57, 106, 161, 200 and 54 (T38260-66)

were identified in transgenic T-cell paradigm and T-cell clone

paradigm searches for genes which are differentially expressed

within and/or among T helper (TH) cell subpopulations. The 54

gene (T38266) is differentially expressed within the THI cells

than in TH2 cells. The 54 gene codes for a novel cysteine protease

(W01048) that may be involved in tissue degradation. It is

possible that inhibition of 54 gene expression and/or 54 gene

" product ectivity in immune disorders involving THI-like cells may
at least 8 contiguous amino acids of MIP fused to a second protein sequence can be used to target MIP, or its peptides, to specific cells tissues. They can be used as a source of MIP in assays and also as immunogen. The MIP encoding nucleic acid is used for expression of recombinant MIP polypeptides and as a source of probes for detecting MIP-related mRNA.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1996 (first entry)
54 gene differentially expressed in T helper cells.
T helper cell; TF-cell; T-cell; T-cell; differential expression; immune disorder; multiple sclerosis; asthma; lepromatous leprosy; diagnosis; therapy; cysteine protease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                ö
                                                                                                                                                                  / Match 6.0%; Score 28; DB 40; Length 1698; Local Similarity 100.0%; Pred. No. 1.36e-09; les 28; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 24; Length 1257;
Pred. No. 1.09e-03;
0; Mismatches 0; Indels (
                                                                                                                             413 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag- c
/note- "base 1147 is given as v in the specification"
                                                                                                                             449 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 G;
                                                                                                                             381 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 C;
                                                                                                                                                                                                                                                       75 ggaattcccgggtcgacccacgcgtccg 102
                                                                                                                                                                                                                                                                                             29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 22..1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serve to minimise tissue damage.
                                                                                                                                                                                                                                                                                                                                                            T
T38266 standard; cDNA; 1257 BP.
                                                                                                                             455 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ccgggtcgacccacgcgtccg 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1996; U02798.
03-MAR-1995; US-398633.
04-UN-1995; US-487748.
(MILL-) MILLENNIUW PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 ccgggtcgacccacgcgtccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
397..1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1698 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1257 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Levinson DA;
WPI; 96-433404/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W01048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9627603-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1996
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp
                                                                                                                                                                                                                Matches
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISHING N, MOSS J, NUMILLINGAIE M, ISCUILYA M, MPI; 94-341862/42.

GTP-binding protein ARDI with ADP-ribosylation factor domain - useful as biochemical and diagnostic reagent Example; Table III, Page 16; 52pp; English.

A novel ARD I protein includes an 18 kDa region that exhibits significant homology to known ADP-ribosylation factors (ARFS) and is called ARD I for ARF domain. CDNA was isolated from a human HL-60 lambda library screened with ARF 2B cDNA and a mixture of oligos denoted XARFC. The insert of Clone no. 76 was sequenced. The insert (bps 706-2365 g779326) included an ORF (1207-1722) encoding an ARF domain of 172 AAs. Oligo JIR was used to screen a human fetal brain cDNA lambda 2AP library. Clones were found contg.
                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1995 (first entry)
Primer SALADTT contg. a 5' SalI site, for the analysis of ARD
                                                             ö
   Length 2055;
                                Pred. No. 1.09e-03;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-OCT-1994.
15-APR-1993; US-049252.
19-APR-1993; US-049473.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Mishima K, MOSS J, Nightingale M, Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                Primer SALADTT contg. a 5' Sall site, for the ar
ADP-ribosylation factor; ARF; ARD 1; primer; ss.
      Score 21; DB 24;
                                                                                                                           21
                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                               079345 standard; cDNA; 36 BP. Q79345;
Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative
                                                                                                                                                            36 ccgggtcgacccacgcgtccg
                                                                                                                           1 ccgggtcgacccacgcgtccg
```

LT 6 T38260 standard; cDNA; 2055 BP.

RESULT

g ô

```
g
            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mohapatra SS;
WPI: 96-201752/21

WPD: 96-201752/21

SCreening of a Parietaria pollen library with antisera to a 14 kDa

SCreening of a Parietaria pollen library with antisera to a 14 kDa

CC CDNA clones encoding allergenic proteins: group I (PJ001)

CC COMPRISES Clones PAR64, PAR16, PAR5, PAR21, PAR48, PAR39 and

CC COMPRISES CLONE PAR19 (129007) encoding 2 isoallergens (R97307-08);

CC COMPRISES CLONE PAR19 (129007) encoding 2 isoallergens (R97307-08);

CC COMPRISES CLONE PAR19 (129007) comprising clones PAR70 and PAR10 (129008-09,

CC COMPRISES CLONE PAR19 (129007) encoding 2 isoallergens sequences, or

CC for prodn. of recombinant allergens useful in the diagnosis and

CC immunotherapy of allergic diseases induced by Parietaria.

Sequence 787 BP; 239 A; 189 C; 167 G; 192 T;
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
nucleotides 7-1826 and 726-3225 of 079326. In this sequence, about 1200 nts preceded the ARF region without a stop codon in the same ORF. To further characterise the 5' terminus of this cDNA, 5'-RACE was carried out with the poly A+ RNA from INR-32 human neuroblastoma cells. The poly A+ RNA from INR-32 human neuroblastoma cells. The products were tailed and subhected to PCR with primers SALAD and SALADTI and JATSTRII. TE was added to the PCR primers SALAD and JKNOT. Following transfection of the reverse primars SALAD and JKNOT. Following transfection of the reverse transcribed, PCR amplified sequences into competent DH5-alpha cells, clones correspondence into ARD i were isolated.
                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1996 (first entry)
Parietaria allergen 9J003 PAR70 cDNA (preliminary sequence).
Allergen, pollen; pollinosis; desensitisation; immunotherapy; vaccine; hayfever; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1996 (first entry)
Paridetaria allergen PJ003 PAR10 cDNA (preliminary sequence).
Allergen; pollen; pollinosis; desensitisation; immunotherapy; vaccine; hayfever; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 21; Length 787;
Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Score 18; DB 13; Length 36;
Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LT 9
T29009 standard; cDNA; 845 BP.
T29009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 8
T29008 standard; cDNA; 787 BP.
                                                                                                                                                                                                                                                                                                                            Query Match
3.9%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.9%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              11 ggtcgacccacgcgtccg 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-707065-A2
17-APR-1996.
24-JUL-1995; 401754.
22-JUL-1994; US-279113.
(UJMA-) UNIV MANITOBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-1996.
24-JUL-1995; 401754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      judaica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parietaria judaica
EP-707065-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parietaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIZE SULT TEST S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
       888888888888888
```

```
Immuno-therapy and desensitisation of allergies userui in thin and therapy and desensitisation of allergies userui in Screening of a Parietaria pollen library with antisera to a 14 kba Screening of a Parietaria pollen library with antisera to a 14 kba pollen protein from Parietaria led to the identification of 3 groups of comprises clones anxed, Parie, Pari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding such proteins, assay for antagonists, etc.

Claim 16; Columns 15-18; 12pp; English.

The present sequence encodes a novel human protein, designated CROC-1.

The protein is an activating protein of promoter of the proto-oncogene

c-fos. The specification describes a mammalian cell line whose cells

contain a recombinant expression vector comprising a reporter operatively

linked to a human c-fos promoter and a second expression vector

comprising a nucleic acid encoding that activates the human c-fos

promoter (e.g. GNC-1). Antigenic fragments of the CROC-1 protein can be

used to prepare antibodies, which are used to assay for or purify the

activating protein. Antagonists of the CROC-1 protein bind to, but do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caps . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1998 (first entry) cDNA encoding human CROC-1 protein. CROC-1: activating protein; promoter; proto-oncogene; c-fos; antagonist; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c-fos Promoter-activating proteins - assay for nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 40; Length 1930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      515 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 21; Length 845;
Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                        DNA encoding Parietaria sp. pollen allergen - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activate, the human c-fos promoter. Sequence 1930 BP; 524 A; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= CROC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LT 10
V16738 standard; CDNA; 1930 BP.
V16738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 ggtcgacccacgcgtccg 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 ggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ggtcgacccacgcgtccg 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 ggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1995; 544900.
08-JUL-1994; US-272412.
(SCHE) SCHERING CORP.
Lin SL, Rothofsky ML;
WPI; 98-239204/21.
P-PSDB; W46892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..516
/*tag=
22-JUL-1994; US-279113.
(UYMA-) UNIV MANITOBA.
                                                                                                                               96-201752/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                     Mohapatra SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5736331-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

RESULT

NAME OF THE PART O

```
Preparation of CDNA from RNA molecules - by annealing CDNA synthesis primer to RNA, synthesising DNA and contacting with novel template switching oligonucleotide

Triang 19 Page 29; 39pp; English.

Claim 9; Page 29; 39pp; English.

Claim 9; Page 29; 39pp; English.

Characteristic template switching oligonucleotides (TSO) used in the method of the invention. The method of the invention is for preparing Characteristic the method of the invention. The method of the invention is for preparing Characteristic complementary to the S'-end of an RNA molecule. The method comprises and synthesising a first DNA strand complementary to at least a portion of the RNA molecule, and contacting the RNA molecule with a TSO having a present of mucleotide sequence at its 5'-end and at least 1 riboquanine residue at its 3'-end, where the TSO binds the 5'-end of the RNA molecule and serves as a template for the extension of the 3'-end of the first DNA strand. The method can be used for the synthesis and cloning of full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Template switching oligonucleotide Na21-G5p.
Template switching oligonucleotide: RNA/DNA hybrid; DNA preparation; CDNA synthesis primer; CDNA cloning; CDNA library construction; ss.
                                                                                                                                                                       \overline{27}-WAR-1991 (first entry) BamHI J-I fragment carrying sequences characteristic of productive pseudorables virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudo-rabies virus nucleotide sequences - used for producing nucleate and probes, antigons and antibodies for distinguishing latent from productive infection Disclosure; Page 21; 27pp; English. The fragment carries sequences characteristic of the productive pseudorables viral genome, and may be used as a probe in diagnosis of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 2; Length 2721;
Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1017 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLON-) CLONTECH LAB INC.
Chenchik A, Diatchenko L, Siebert P, Zhu Y;
WPI; 97-363690/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1007 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 A;
    141 ctctcttcccccccct 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ctctctttccccccct 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T98445 standard; DNA; 26 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
                      96 ctctcttccccccct 79
                                                                                                                              Q10212 standard; DNA; 2721
Q10212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1990; 238940.
13-JUN-1990; US-537855.
(USDA ) US AGRIC RES SERV.
Cheung AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22..26
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JAN-1996; US-582562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2721 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-1997.
03-JAN-1997; U00368
                                                                                                                                                                                                                                                               Pseudorables virus.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 91-021957/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_base
                                                                                                                                                                                                                                                                                  US7537855-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09724455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T98445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                           ç
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalian cell lines contg. recombinant vectors encoding c-fos promoter activating proteins - used to identify nucleic acids rencoding stgnal transducing molecules which activate promoters.

Promoter activating proteins - used to identify nucleic acids rencoding stgnal transducings molecules which activate promoters.

CROC-1 cDNA encodes a c-fos promoter activating protein of approx. 19 kD with an acidic amino terminal half and a basic carboxy terminus. The crotein includes a kinase target domain which contains phosphorylation sites for a variety of kinases involved in signal transduction. CROC-1 mRNA is approx. 2.3 kb in length and present in all tissues examined. The cDNA is used in vectors, operatively linked to a nucleic acid encoding a polyomavirus large T antigen. Mammalian cell lines contg. these vectors, and vectors comprising a polyoma origin of replication and a nucleic acid suspected to encode and activating protein of the promoter, can be used to identify signal transducing molecules.

Sequence 1930 BP; 524 A; 487 C; 404 G; 515 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                    T15610;
25-JUN-1996 (first entry)
CROC-1 CDNA encodes c-fos promoter activating protein.
CROC-1; CROC-4; c-fos promoter activating protein; signal transducer;
polyomavirus large T antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudo-rablies nucleotide sequences - used for producing nucleic acid probes, antigens and antibodies for distinguishing latent from productive infection.

Disclosure; Page 22; 27pp; English.

The fragment carries sequences characteristic of the latent pseudorables viral genome, and may be used as a probe in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BamHI J-I fragment carrying sequences characteristic of latent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 18; Length 1930;
Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 2; Length 2721;
Pred. No. 2.20e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1017 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1007 C;
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                  /*tag= a
/product= CROC-1
.T 11
T15610 standard; cDNA; 1930 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 12
Q10543 standard; DNA; 2721 BP.
Q10543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.9%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.9%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 ggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-1990.
13-JUN-1990: 238940.
13-JUN-1990: US-537855.
(USDA ) US AGRIC RES SERV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 ggtcgacccacgcgtccg 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                 05-JUL-1995; U07874.
08-JUL-1994; US-272412.
(SCHE) SCHERING CORP.
LIN SL, ROTHOFSKY ML;
WPI; 96-097629/10.
P-PSDB; R90769.
                                                                                                                                                                                                1..516
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2721 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pseudorabies virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudorables virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 91-021957/03.
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US7537855-A.
                                                                                                                                                                                                                                                                                    25-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheung AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

RESULT

g õ ö

Gaps

```
Mishima K, Moss J., Nightingale M, Tsuchiya M;

WPI: 94-341862/42.

TP-binding protein ARD1 with ADP-ribosylation factor domain -

useful as biochemical and diagnostic reagent

Example; Table III, Page 16; 52pp; English.

Example; Table III, Page 16; 52pp; Table III, English.

Example; Table III, Page 16; 52pp; Table III, English.

Example; Table III, Page 11; 52pp; Table III, English.

Example; Table III, Page 11; 52pp; Table III, English.

Example; Table III, Page III, Page III, English.

Example; Table III, English.

Example; Table 
length cDNA, or fragments, that correspond to the complete sequence of the 5'-end of the mRNA molecule. It can be used to construct cDNA libraries from nanogram quantities of total or poly A+ RNA. The TSO allows for negative selection against cDNA that are not complementary to the 5'-end of the template RNA, while allowing full length cDNA to be readily selected: 8 A; 3 C; 12 G; 3 T;
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                 Score 17; DB 36; Length 26;
Pred. No. 1.17e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 13; Length 35; Pred. No. 1.17e+00; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1995 (first entry)
Primer SALAD for the analysis of ARD 1.
ADP-ribosylation factor; ARF; ARD 1; primer; ss.
Synthetic.
W0944283-A.
27-0CT-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH) US DEPT HEALTH & HUMAN SERVICES.
Mishima K, Moss J, Nightingale M, Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 15
Q79346 standard; cDNA; 35 BP.
Q79346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%;
Local Similarity 100.0%;
nes 17; Conservative
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                    10 aagacgacagaaggggg 26
                                                                                                                                                                                                                                                                                                                                                                15-APR-1994; U04190.
16-APR-1993; US-049252.
19-APR-1993; US-049473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8888888
                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                          ò
```

Search completed: Mon Mar 8 23:40:43 1999 Job time : 314 secs. 40 gtcgacccacgcgtccg õ

19 gtcgacccacgcgtccg 35

g

Best Loc Matches

ö

Gaps

ő

0; Indels

		(MI)
'	 	
'== 	' '-	:::: []
<u> '-</u>	 	: <u>-</u> '.] ~
-		
	- <u> </u>	· -]
	-	
	 >}	

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Mon Mar 8 23:41:01 1999; MasPar time 35.32 Seconds 1148.278 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-206-040-1 (1-469) from US09206040A.seq 465

1 traacttgcagcgnccaggt........gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca........ctactatgtaacttctanna Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE jmetric Gap 60 Scoring table:

Dbase 0; Query 0 Nmatch STD

165359 seqs, 43243793 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

n-issued 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 6.835; Variance 2.301; scale 2.970

Statistics:

SUMMARIES

LIBRARY: Prostrate TOPOLOGY: linear MOLECULE TYPE: CDN IMMEDIATE SOURCE:

1.556 01 1.556 01 1.556 01 1.556 01 1.556 01 1.556 01 1.556 01 2.746 01
Application
6,2,2,4,1,1,3,4,0,0,0,0,1,1,4,6,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1
Sednence Sed
PCT-US95-0 US-08-073- US-08-568- US-08-487- US-08-407- US-08-407- US-08-407- US-08-407- US-08-467- US-08-544- US-08-544- US-08-544- US-08-544- US-08-544- US-08-544- US-08-544- US-08-544- US-08-544- US-08-548- US-08-788- US-08-
4HMM08M0040M000M000M0044H4
1700 12883 12888 1600 1700 1800 1800 1800 1800 1800 1800 18
44444444444444444444444444444444444444
0000 0000

ALIGNMENTS

Sequence 1, Application US/08633682
C Sequence 1, Application US/08633682
C Sequence 1, Application US/08633682
C Patent No. 5840544
C GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R. APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: BANDENCE LAND E.
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 23174 Porter Drive
CITY: Palo Alto COUNTRY: U.S.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPOTER: IBM Compatible
OOFERATING SYSTEW. DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,682
FILING DATE: Filed Herewith
ATTORNEY/AGENT: Filed Herewith
ATTORNEY/AGENT: RIBCRAMION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0063 US
TELEPAN: 415-855-0195
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```
Sequence 2, Application US/08785065
Patent No. 5814451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIAL COURT COURT CONF. CONSENS
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                     Palo Alto
                                                                                                                                           USA
                                                                                                                                          COUNTRY: US
                                                                                                           STREET:
CITY: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
  ò
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Stuart, Susan G.
APPLICANT: MITTY, Lynn E.
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 3; Length 969;
Pred. No. 1.25e-11;
0; Mismatches 0; Indels
                              Score 28; DB 3; Length 570;
Pred. No. 1.25e-11;
0; Mismatches 0; Indels
CLONE: 836820
SEQUENCE 570 BP: 149 A: 155 C: 137 G: 129 T: 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 775426
SEQUENCE 969 BP; 163 A; 324 C; 280 G; 202 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-785-065-2 STANDARD; DNA; UNC; 1023 BP
                                                                                                                               .r 2
US-08-700-637-1 STANDARD; DNA; UNC; 969 BP
                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/700,637
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0065 US
                                                                         59 GGAATICCCGGGTCGACCCACGCGTCCG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                         Sequence 1, Application US/08700637
Sequence 1, Application US/08700637
Patent No. 5854413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0155
TELEPHONE: 415-82-0195
INPORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Luther, Barbara J. REGISTRATION NUMBER: 33,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                               Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLUNOT05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDN2
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIALL
LIBRARY: COLM...
775426
                                                                                                                                                                                                                                                                                                                               U.S.
                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: U
```

Sequence 2, Application US/08785065

g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08726575A
Sequence 1, Application US/08726575A
Sequence 1. Application US/08726575A
Sequence 1. Application US/08726575A
Sequence 1. Sequence 2. Sequence 3. Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
APPLICANT: Bandman, olga
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTON: NOVEL SUBUNITS OF NADH DEHYDROGENASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1023 BP; 217 A; 270 C; 290 G; 246 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 3; Len
Pred. No. 1.25e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FRATESC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,065
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 4
US-08-726-575A-1 STANDARD; DNA; UNC; 1529 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0187 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 GGAATTCCCGGGTCGACCCACGCGTCCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              King of Prussia
```

```
Sequence 1, Application US/08460898
Sequence 1, Application US/08460898
C Sequence 1, Application US/08460898
C Patent No. 5850022
C GENERAL INFORMATION:
C APPLICANT: Dehesh, Katayoon
APPLICANT: Dehesh, Toni Alois
APPLICANT: Hawkins, Deborah
APPLICANT: Hawkins, Deborah
APPLICANT: Hawkins, Perduction of Myristate in Plant Cells
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calyee, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMMUNICATION: 95616
COMMUNICATION: 95616
COMMUNICATION: 195616
COMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
6.0%; Score 28; DB 2; Length 1581;
Best Local Similarity 100.0%; Pred. No. 1.25e-11;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA tO MRNA
SEQUENCE 1581 BP; 418 A; 356 C; 410 G; 397 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,898
FILING DATE: 05-UN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: 08/383,756
FILING DATE: 02-FEB-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: 08-7816
FILING DATE: 02-FEB-1995
CLASSIFICATION NUMBER: 08-7816
FILING DATE: 02-FEB-1995
CLASSIFICATION NUMBER: 08-7816
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29-0CT-93
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-0CT-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scheerer
REGISTRATION NUMBER: 34,719
NAME: CATI J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 111
TELECOMMNINCATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-460-898-1 STANDARD; DNA; UNC; 1581 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 GGAATTCCCGGGTCGACCCACGCGTCCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/261,695 FILING DATE: 16-JUN-94
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08383756
Sequence 1, Application US/08383756
Sequence 1, Application US/08383756
C Patent No. 5654495
C GENERAL INFORMATION:
APPLICANT: Dehesh, Katayoon
APPLICANT: Hawkins, Deborah
APPLICANT: Hawkins, Deborah
APPLICANT: Devies, Huw Maelor
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%; Score 28; DB 3; Length 1529; Best Local Similarity 100.0%; Pred. No. 1.25e-11; Matches 28; Conservative 0; Mismatches 0; Indels
                  ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: No
SEQUENCE 1529 BP; 390 A; 374 C; 315 G; 450 T; 0 OTHER.
                                                                                              COMPUTER: 16M 400

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,575A
FILING DATE: OCTOBER 8, 1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATORNEY/AGENT INFORMATION:
NAME: William T. HBA
RECISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG 50025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 4026
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1(a)
CURBUT APPLICATION DATA: US/08/383,756
FILING DATE: 02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 5
US-08-383-756-1 STANDARD; DNA; UNC; 1581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 GGAATICCCGGGTCGACCCACGCGTCCG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,695
FILING DATE: 16-JUN-94
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA
USA
            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
              ò
```

<u>:</u>

Gaps

ö

Gaps

```
Sequence 3, Application US/08487748A
GENERAL INFORMATION:
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                 4.5%; Score 21; DB 2; Length 1257; Best Local Similarity 100.0%; Pred. No. 5.73e-05; Watches 21; Conservative 0; Mismathle
                                                                                                                                      NAME/KEY: CDS
LOCATION: 22..1137
SEQUENCE 1257 BP; 323 A; 357 C; 323 G; 253 T; 1 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/487,748A FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                          .T 8
US-08-487-748A-3 STANDARD; DNA; UNC; 2055 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7853-023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUGA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-(
TELEPOMUNICATION INFORMATION:
TELEPONE: (212) 790-9090
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2055 base pairs
      11:
   INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                          1 CCGGGTCGACCCACGCGTCCG 21
                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                   TOPOLOGY: unknown MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                           XXXXXX
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                          셤
      8888888888888
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 3; Length 1581
Pred. No. 1.25e-11;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
SEQUENCE 1581 BP; 418 A; 356 C; 410 G; 397 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-487-748A-11 STANDARD; DNA; UNC; 1257 BP
                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/968,971
FILING DATE: 30.0CT-92
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: COIUZZI, LGAUEZ, 1, 1242
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-023
TELECOMMUNICATION INFORMATION:
TELEDBIONE: (212),790-9990
TELEFAX: (212) 869-8864/9741
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29-OCT-93
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/487,748A FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 GGAATICCCGGGTCGACCCACGCGTCCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
ö
                                                                                          Gaps
                                                                                          ö
                                                  Score 21; DB 2; Length 2055;
Pred. No. 5.73e-05;
0; Mismatches 0; Indels
LOCATION: 496..1509
SEQUENCE 2055 BP; 623 A; 460 C; 415 G; 557 T; 0 OTHER.
                                                  4.5%;
Best Local Similarity 100.0%;
Matches 21; Conservative
```

셤 ò XXXXXX

```
APPLICANT: Nightingale, Maria
APPLICANT: Tsuchiya, Mikako
TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLECTIDE BINDING
TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITT: NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application PC/TUS9404190
Sequence 20, Application PC/TUS9404190
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary, Department APPLICANT: of Health and Human Services TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 1; Length 30;
Pred. No. 2.33e-02;
....arthes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR CITY: NEWPORT BEACH STATE: CA COUNTRY: USA ZIP: 92660 COMPUTER READABLE FORM:
                                                                                                                                                                                       ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/312,648
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,473
FILING DATE: 19-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: FULIOR, MICHAEL L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH050.001DV1
TELEPHONE: 619-235-6550
TELEPHONE: 619-235-650
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
ENGTH: 36 base pairs
TELEGHH : 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
SEQUENCE 36 BP; 4 A; 12 C; 11 G; 9 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UT 11
PCT-US94-04190-20 STANDARD; DNA; UNC; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GTCGACCCACGCGTCCGT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 gtcgacccacgcgtccgt 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CE
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                            COUNTRY:
                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                 Sequence 20, Application US/08049473
GENERAL INFORMATION:
APPLICANT: Mishina, Koichi
APPLICANT: TSuchiya, Misko
TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING
TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRIE COUNTRIE COUNTRIE COUNTRIE COUNTRIE COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,473
TITING DATE: 19930419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 1; Length 36;
Pred. No. 2.33e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19930419
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH050.001CP1
TELEPHONE: 619-235-850
TELEPHONE: 619-235-850
TELEPHONE: 619-235-850
TELEPHONE: 619-235-850
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
SEQUENCE 36 BP; 4 A; 12 C; 11 G; 9 T; 0 OTHER.
                                                                                    RESULT 9
ID US-08-049-473-20 STANDARD; DNA; UNC; 36 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .T 10
US-08-312-648-20 STANDARD; DNA; UNC; 36 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08312648
Sequence 20, Application US/08312648
Patent No. 5514600
GENERAL INFORMATION:
APPLICANT: MOSS, JOel
APPLICANT: Mishima, Koichi
Query Match 3.9%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 GTCGACCCACGCGTCCGT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 gtcgacccacgcgtccgt 57
                                                                                                                                                                                                                                                                                                                                                                                                     NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CA
```

RESULT

g ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1930;
                                                                                                   APPLICANT: Lin, Stanley Li
APPLICANT: Rothofsky, Marnie Lynn
TITLE OF INVENTION: Method for Identifying Nucleic
TITLE OF INVENTION: Acids Encoding c-fos Promoter
TITLE OF INVENTION: Acids Encoding Proteins
NUMBER OF SEQUENCES: 3
CORRESPEE: Schering-Plough Corporation
ADDRESSEE: Patent Department K-6-1 (1990)
STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; DB 2; Length 1930
Pred. No. 2.33e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C XXXXXX
OI JAN-1900
DE Patent No. 5215881.
C Patent No. 5215881.
C Patent No. 5215881.
C TITLE OF INVENTION: PSEUDORABIES DIAGNOSIS PROBES NUMBER OF SEQUENCES: 3
C CURRENT APPLICATION DATA:
C APPLICATION NUMBER: US/07/537,855
FILING DATE: 13-JUN-1990
C SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
SEQUENCE 1930 BP; 524 A; 487 C; 404 G; 515 T; 0 OTHER.
   US-08-544-900-1 STANDARD; DNA; UNC; 1930 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,412
FILING DATE: 8-JUL-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Thompson, Paul A.
REGISTRATION NUMBER: 35,385
                                                                                                                                                                                                                                                                               ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SSOFTWARE: Microsoft Word F.
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OC0439K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5215881-2 STANDARD; DNA; UNC; 2948 BP
                                          Sequence 1, Application US/08544900 Sequence 1, Application US/08544900 Patent No. 573631 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: OC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 5150
TELEFRX: 908 298 5388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1930 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%;
Local Similarity 100.0%;
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 GGTCGACCCACGCGTCCG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 ggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                      CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                  XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
    Sequence 1, Application PC/TUS9507874
Sequence 1, Application PC/TUS9507874
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for Identifying Nucleic Acids Encoding c-fos Promote NUMBER OF SEQUENCES: 2
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION NUMBER: PCT/US95/07874
FILING DATE: -June-1995
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 4; Length 1930;
Pred. No. 2.33e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 4; Length 36;
Pred. No. 2.33e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE 1930 BP; 524 A; 487 C; 404 G; 515 T; 0 OTHER.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04190
                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH050.001QPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-0176
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
SEQUENCE 36 BP; 4 A; 12 C; 11 G; 9 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 12
PCT-US95-07874-1 STANDARD; DNA; UNC; 1930 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,412
FILING DATE: 8-UUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGHT: 1930 base pairs
TYPE: nucleic acid
STRANEEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GTCGACCCACGCGTCGT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 ggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 gtcgacccacgcgtccgt 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GGTCGACCCACGCGTCCG 72
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
```

엄 δŏ ö

g δλ

```
Sequence 21, Application US/08049473
Sequence 21, Application US/08049473
Sequence 21, Application US/08049473
CC GENERAL INFORMATION:
CREMEAL INFORMATION:
CREMEAL INFORMATION:
CREMEAL INFORMATION:
CC APPLICANT: Mishina, Noichi
APPLICANT: Wishina, Noichi
APPLICANT: PSUCHICANTON: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN
UNDERSONE: PROPERING PROPERING PROPERING STREEN:
CORRESSONE: REDORNER SEARCH
CORRESSONE: RESERVENCE OF THE REDORNER SEARCH
CORRESSONE NUMBER: 36,516
CRESSERVENCE CARACTER SEARCH
CREECANDUNICATION NUMBER: 36,516
CREECONMUNICATION NUMBER: 36,516
CREECONTRIBUTION NUMBER: 36,516

                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                        Score 18; DB 5; Length 2721;
Pred. No. 2.33e-02;
0; Mismatches 0; Indels
LENGTH: 2721
Sequence 2948 BP; 428 A; 1007 C; 1017 G; 269 T; 227 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 1; Length 35;
Pred. No. 1.55e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE 35 BP; 4 A; 12 C; 11 G; 8 T; 0 OTHER.
                                                                                                                                                                                                                                             .T 15
US-08-049-473-21 STANDARD; DNA; UNC; 35 BP.
xxxxxxx
                                                                                                                                      Query Match
3.9%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.7%;
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GTCGACCCACGCGTCCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 gtcgacccacgcgtccg 56
                                                                                                                                                                                                                                           ပ္ပင္တ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                          g
```

Search completed: Mon Mar 8 23:42:51 1999 Job time: 110 secs.

THIS PAGE BLANK (USPTO)

	//
‡ ' <u>-</u>	<u> </u>
[
:	

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Mon Mar 8 23:10:19 1999; MasPar time 622.20 Seconds 1349.844 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Run on:

Tabular output not generated.

1 traacttgcagcgnccaggt.......gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.......ctactatgtaacttctanna >US-09-206-040-1 (1-469) from US09206040A.seq 465 Description: Perfect Score: N.A. Sequence: Comp: Title:

Scoring table:

Dbase 0; Query 0 TABLE jmetric Gap 60 Nmatch STD 2275026 seqs, 895388244 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est56 Database:

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est109 5:qp_est1 6:qp_est10 7:qp_est11 8:qp_est12 9:qp_est13 10:qp_est14 11:qp_est15 12:qp_est16 13:qp_est17 14:qp_est18 15:qp_est19 16:qp_est2 17:qp_est20 18:qp_est21 19:qp_est3 20:qp_est4 21:qp_est5 22:qp_est6 23:qp_est7 24:qp_est8 25:qp_est9 26:qp_gss1 27:qp_qss2 28:qp_gss3 29:qp_gss4 Database:

Mean 8.493; Variance 1.124; scale 7.553 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

: 2222		. മമമമമെ			. ннининич		rane rane rane rane rane
5C04F08-T7 mer 5C06d02-t7 mer 5C06h03-t7 mer 5C06a03-t7 mer	5C04F08-T7 memt 5C06d02-t7 memt 5C06h03-t7 memt 5C06a03-t7 memt 5C06a03-t7 memt	5C04F08-T7 meml 5C06d02-t7 meml 5C06h03-t7 meml 5C06a03-t7 meml 5C06g03-t7 meml HOMO sapiens mi	5C04F08-T7 ment 5C06d02-t7 ment 5C06h03-t7 ment 5C06a03-t7 ment 5C06a03-t7 ment HOMC Sapiens mi 5C01e04-t7 ment 5C01e04-t7 ment	5C04F08-T7 memb) 5C06d02-t7 memb) 5C06d03-t7 memb) 5C06d03-t7 memb) 5C06g03-t7 memb) Home sapiens mR 5C01E04-t7 memb) 5C06h05-t7 memb)	5004F08 T7 membr 5006d02-t7 membr 5006d03-t7 membr 5006d03-t7 membr 5006g03-t7 membr Homo sapiens mRk 501e04-t7 membr 5006h05-t7 membr 5006h05-t7 membr 5006h05-t7 membr	5C04F08-T7 membra 5C06d02-t7 membra 5C06d03-t7 membra 5C06g03-t7 membra 6C06g03-t7 membra Homo sapiens mRNA 5C01e04-t7 membra 5C04E02-T7 membra 5C04E02-T7 membra 5C0610-t7 membra	5CC4FO8-T7 membrane-fr 5cO6AO2-t7 membrane-fr 5cO6AO3-t7 membrane-fr 5cO6AO3-t7 membrane-fr 5cO6GO3-t7 membrane-fr Homo sapiens MRNA; exp 5cO1EO4-t7 membrane-fr 5cO6AO5-t7 membrane-fr 5cO6EO3-T7 membrane-fr 5cO6CIO-t7 membrane-fr 5cO6CIO-t7 membrane-fr
5C04F08 5C06d02 5C06d03	5C04F08 5C06d02 5C06h03 5C06a03	5C04F08- 5C06d02- 5C06h03- 5C06a03- 5C06g03- HOMO Sab	5C04F08-5 5C06d02-5 5C06d03-5 5C06g03-7 HOMO SAP	5C04F08-5 5C06d02-5 5C06a03-5 5C06g03-7 HOMO Sap 5C01e04-5	5C04F08-5 5C06d02-5 5C06d03-5 5C06d03-6 FOMO Sap FOMO Sap 5C01e04-6 5C01e04-6 5C04E02-6	5004F08-5 5006d02-5 5006d03-5 5006d03-5 5006d03-5 5001e04-5 5001e04-5 5006c10-5	5C04F08- 5C06d02- 5C06d03- 5C06d03- F0m0 sap Homo sap 5C01e04- 5C04E02- 5C04E02- 5C04E02- 5C04E02-
5006	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	5006 5006 5006 5006 5006	5006 5006 5006 5006 5001	5006 5006 5006 5006 5001 5001	5006 5006 5006 5006 5001 5001 5006	00000000000000000000000000000000000000	50000000000000000000000000000000000000
5006	5000 5000 5000 5000	5006 5006 5006 HOMO	50061 50061 50061 10000	5006 5006 5006 5001	5001 5006 5001 5006 5001 5006	50000000000000000000000000000000000000	50000000000000000000000000000000000000
5c06h0 5c06a0	5c06h0 5c06a0 5c06a0	5c06h0 5c06a0 5c06g0 Homo s	5c06h0 5c06a0 5c06a0 5c06g0 Homo s	5c06h0 5c06a0 5c06g0 Homo s 5c01e0	5c06h0 5c06a0 5c06a0 Homo s 5c01e0 5c06h0	5c06h0 5c06a0 5c06g0 Homo s 5c01e0 5c06h0	5c06h0 5c06a0 5c06a0 5c06a0 5c01e0 5c06h0 5c06c1
5c06a03-	5c06a03-	5c06a03- 5c06g03- Homo sap	5c06a03- 5c06g03- Homo sap 5c01e04-	5c06a03- 5c06g03- Homo sap 5c01e04- 5c06h05-	5006903- 5006903- Homo sap 501e04- 5006h05-	500603- 500603- Homo sap 501e04- 500605- 500605-	500603- 500603- Homo sap 501e04- 500605- 500405- 500405-
	5c06q03-t7	5c06g03-t7 Homo sapier	5c06g03-t7 Homo sapier 5c01e04-t7	5c06g03-t7 Homo sapier 5c01e04-t7 5c06h05-t7	5c06903-t7 Homo sapier 5c01e04-t7 5c06h05-t7 5C04E02-T7	5c06g03-t7 Homo sapier 5c01e04-t7 5c06h05-t7 5c04E02-T7	500693-t7 Homo sapier 501e04-t7 5006h05-t7 5004E02-T7 5006c10-t7

Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
fax: 602-621-7186
E-mail: helnjars@ccit.arizona.edu

Chris Baysdorfer Department of Biological Sciences, School of Science California State University, Hayward Hayward, CA 94542

	.72e-
177 membra bbda-PR12 bbda-x8353 177 membra	64 Finds radiata Somat GDMO0L03 human embryo GDMO0L05 human embryo
HSU46350 118713 HSU46349 118706349 1118706 1118706 1118295 1118295 1118299 1118299 1118299 1118299 1118299 1118299 1118299 1118299 1118299 1118299 1118299 1118299 1118290 1118290 1118274 1118274 1118274 1118274 1118274	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	95 11 6
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	8 8 8 7 7 7
0 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 4 U 4 12

ALIGNMENTS

```
libraries
Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <1. .>214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Conservative
ph: 602-6218-746
fax: 602-621-7186
                                                                           Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
T18319
g463352
                                                                                                                                                                                                                               Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
G
                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
/strain="W64A2"
/note="Vector: ZipLox: Site_1: Sall; Site_2: Notl; ds-cDNA
/note="Vector: ZipLox: Site_1: Sall; Site_2: Notl; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
Notl oligo- dT oligomer and then adding the second strand
to RNase-nicked DNA:RNA hybrid with DNA Poll. Sall
adaptors were added to the ends, the ds-cDNAs were then
digested with Notl and size-selected. These were
directionally-cloned into the ZipLox phage vector, excised
as plasmids, and then individually analyzed."
/clone="Scottor"
/clone="Scottor"
/lab_nose="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 214)
Shen, B., Carnelro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T18296 214 bp mRNA EST 17-OCT-1996 5C06d02-t7 membrane-free polysomes from endosperm Zea mays CDNA clone 5C06d02 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                               for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 21; 1
Pred. No. 3.59e-31;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Mol. Biol. 26, 1085-1101 (1994)
95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 t
                                       E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                 E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 ggaattcccgggtcgacccacgcgtccgta 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 GGAATICCCGGGTCGACCCACGCGTCCGTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: The Maize cDNA Project
                                                                                             Interdisciplinary Center for
DNA Sequencing Core
University of Florida
P.O. Box 100695
Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                       Seq primer: T7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .>568
a 183 c
                   510-727-2035
   ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ibraries
                                                                             Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
```

RESULT

ò

```
/organism="Zea mays"
/strain="W64A2"
/note="Vector: ZipLox; Site_1: Sall; Site_2: NotI: ds-rDN:
was prepared from oligo-dr selected mRNA by priming with was prepared from oligo-dr selected mRNA by priming with to RNase-nicked DNA:RNA hybrid with DNA Poll: Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."
/db.xrefe"taxon:4577"
/clone_scode02*
/lab_bost="DH10B"
/lab_bost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-1996 5006h03-t7 membrane-free polysomes from endosperm Zea mays CDNA clone 5c06h03 5' end similar to ribosomal protein S8, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                Department of Biological Sciences, School of Science California State University, Hayward Hayward, CA 94542 Ph: 510-813-3459 fax: 510-727-2035
                                                                                                                                                                                                                                                                                                        Interdisciplinary Center for Biotechnology Research DNA Sequencing Core University of Florida P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 21; Length 214
Pred. No. 8.16e-29;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                    E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GGAATICCCGGGTCGACCCACGCGTCCGT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 ggaattcccgggtcgacccacgcgtccgt 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρ
                                                                                                                                                                                                                                                                                                                                                                                                                               Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
```

MEDLINE

```
RESULT
LOCUS
                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                     SOURCE
                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                      ACCESSION
                                                                                                                                        DEFINITION
                                     ORGANISM
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                           9 GGAATTCCCGGGTCGACCCACGCGTCCGT 37
                                                                                                                                                                                                                        T18280 407 bp mRNA EST 5c06a03-t7 membrane-free polysomes from endosperm clone 5c06a03 5' end, mRNA sequence.
                                                                     g463313
EST.
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnoliop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer:
                                   Zea mays
                                                      maize
                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                           6.2%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson,
ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interdisciplinary Center for Biotechnology Research DNA Sequencing Core University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biological Sciences, School California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
NotI oligo- dT oligomer and then adding the second strand
to RNase-nicked DNA: RNA hybrid with DNA PolI: SalI
adaptors were added to the ends, the ds-cDNAs were then
digested with NotI and size-selected. These were
directionally-cloned into the ZipLox phage vector, excised
as plasmids, and then individually analyzed."
/db_xref="taxon:4577"
/clone="5c06h03"
/clone="5c06h03"
/clone="b#H0B"
/lab_host="pH10B"
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism-"Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA 94542
                                                                                                                                                                                                                                                                                                                                                                               .>331
78 c
                                                                                                                                                                                                                                                                                                         Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                               103
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                             DB 21;
8.16e-29;
                                                                                                                                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                         Length 331;
                                                                                                                                                                                                                                                                                                                                                                             12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Science
Magnoliophyta;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                    Zea mays cDNA
                                                                                                                                                      17-OCT-1996
                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85723
                                                                                                                                                                                                                                                                                           0
                 LOCUS
                                                                                   ş
                                                                                                                     밁
 DEFINITION
```

```
MEDLINE
COMMENT
                                                                                                                                                                      mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                   Query Match 6.2%;
Best Local Similarity 100.0%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
    29
                     GGAATTCCCGGGTCGACCCACGCGTCCGT 35
ggaattcccgggtcgacccacgcgtccgt 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liliopsida; Poales; Poaceae; 1 (bases 1 to 407)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interdisciplinary Center
DNA Sequencing Core
University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept. of Plant So
ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biological Sciences, School of California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fax: 602-621-7186
E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, Az, 85721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helentjaris TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ibraries
                                                                                                                                                                                              113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Plant
                                                                                                                                                                                                                                                                          /note-"Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA PolI. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

/db_xref-"taxon.4577"
                                                                                                                                                                                                                                   /clone_lib="membrane-free polysomes
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism-"Zea mays"
                                                                                                                                                                                            .>407
80 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (primary contact)
Sciences
                                                                                                                                                                                              ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1085-1101 (1994)
                                                                                Score 29; DB 21; Le
Pred. No. 8.16e-29;
0; Mismatches 0;
                                                                                                                                                                                       95 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for Biotechnology Research
                                                                                                                                                                                              119 t
                                                                                                                        Length 407;
                                                                                     Indels
                                                                                                                                                                                                                                                         from endosperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                     0..
                                                                                     Gaps
```

5c06g03-t7 membrane-free

439 bp

mRNA

polysomes from endosperm

Zea mays cDNA

T18310

```
mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
  Query Match
Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone !
T18310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays

Eukaryotae; mitochondrial eukaryotes; Viridiplantae;

Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;

Liliopsida; Poales; Poaceae; Zea.

1 (bases 1 to 439)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreer.
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J.
h 6.2%;
Similarity 100.0%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Mol. Biol. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial sequencing and mapping of clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g463343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Arizona
Dept. of Plant Sciences, University of Arizona,
ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jarkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interdisciplinary Center for Biotechnology Research DNA Sequencing Core University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biological Sciences, School of Science California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helentjaris TG (primary Dept. of Plant Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ibraries
                                                                                                   108
                                                                                                                                  /notes "vector: ZipLox; Site_1: Sall; Site_2: Notl; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a Notl oligo-dT oligomer and then adding the second strand to RNAse-nicked DNA:RNA hybrid with DNA Poll. Sall adaptors were added to the ends, the ds-cDNAs were then digested with Notl and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

/clone_1b="maxon:4577"
/clone_lib="membrane-free polysomes from endosperm"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5c06g03 5′
                                                                                                                      <u>^</u>
                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end, mRNA sequence.
                                                                                                   o
Score
Pred.
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1085-1101 (1994)
                                                                                                   101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contact)
re 29; DB 21; I
d. No. 8.16e-29;
Mismatches 0;
                                                                                                   g
                                                                                                   96
                                                                                                   rt
    0
                                  Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from two maize cDNA
                                                                                                   11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tucson,
  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCreery,T.,
abben,J. and
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ,
  0,
```

```
REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
ORGANISM
                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                           RESULT
LOCUS
               COMMENT
                                                                                                                                                                                                                                                                                                                                                    င္ပ
                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                       TITLE
                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                 ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggaattcccgggtcgacccacgcgtccgt 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAATTCCCGGGTCGACCCACGCGTCCGT 41
                                                                                                                                                                                                                    g463290
EST.
                                                                                                                                                                                                                                                 clone
T18257
                                                                                                                              Eukaryotae; mitochondrial eukaryotes; viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 113)
                                                                                                                                                                                                      maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-SEP-1997) Korn B., Institution Molekulare
Genomanalyse, Deutsches Krebsforschungszentrum Heidelberg,
Neuenheimer Feld 506, D-69120 Heidelberg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korn,B., Wiemann,S., Ebert,L. and Poustka,A. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; Metazoa; (
Primates; Catarrhini;
1 (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens mRNA;
3' read, mRNA seque
Contact: The Maize cDNA Project
                            Plant Mol. Biol.
95111093
                                                                                                                 Shen, B.,
                                                                                                                                                                                         Zea mays
                                                                                                                                                                                                                                                                              5c01e04-t7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST; expressed sequence
                                                                    Partial sequencing and mapping of clones
                                                                                               Helentjaris,T., Baysdorfer,C., Almira,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Korn, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z99396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSZ99396
                                                                                                                                                                                                                                                                                                                                                                                                            h 6.2%;
Similarity 100.0%;
29; Conservative
                                                        libraries
                                                                                     arkins, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
                                                                                                                                                                                                                                                             7 113 bp mRNA
04-t7 membrane-free polysomes from
5c01e04 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=lib="DKFZphamy1"
/clone="DKFZphamy1_1c11"
/tissue_type="amygdala"
/dev_stage="adult"
a 156 c 151 g 120
                                                                                                                Carneiro, N., Torres-Jerez, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 bp
                                        26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Vertebrata; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 9; 1
Pred. No. 8.16e-29;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tag; clone DKFZphamy1_1c11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                 Stevenson,R., McCreery,T.,
E., Ferl,R., Habben,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 589
                                                                                                                                                                                                                                                                            endosperm
                                                                     from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                           Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ħ
                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

Helentjaris TG (primary of Dept. of Plant Sciences University of Arizona Dept. of Plant Sciences,

contact)

University of Arizona, Tucson, AZ, 85727

```
mRNA
BASE COUNT
ORIGIN
                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                       RESULT 8
LOCUS
DEFINITION
                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
JOURNAL
MEDLINE
                                                        TITLE
                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GGAATTCCCGGGTCGACCCCACGCGTCCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                 ggaattcccgggtcgacccacgcgtccg
                                                                                                                                                                                                                                                                                             T18320 114 bp mRNA 5c06h05-t7 membrane-free polysomes from clone 5c06h05 5' end, mRNA sequence.
 Plant Mol. Biol.
95111093
                                                                                      Shen, B., Carneiro, N., Torres-Jerez, I., Ste Helentjaris, T., Baysdorfer, C., Almira, E.,
                                                                                                                             Eukaryotae; mitochondrial eukaryotes; viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida: Poales; Poaceae; Zea.
1 (bases 1 to 114)
                                                                                                                                                                                                                                                                  g463353
                                                    Partial sequencing and mapping of clones from two maize cDNA
                                                                      Larkins, B.
                                                                                                                                                                                                       Zea mays
                                                                                                                                                                                                                           maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 6.0%;
Similarity 100.0%;
28; Conservative
                                     ibraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing Core
University of Florida
P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biological Sciences, School of Science California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-mail: cbaysdor@sl.csuhayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interdisciplinary Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602-6218-746
: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligomer and then adding the second strand to RNAse-nicked DNA:RNA hybrid with DNA PolI. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

/db_xref="taxon:4577"
/clone="ib="membrane-free polysomes from endosperm"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                 26,
                 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 2: Pred. No. 1.72e: 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
1.72e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                      Stevenson,R., McCreery,T.,
E., Ferl,R., Habben,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                     endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
```

οy В

```
KEYWORDS
                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                              29 ggaattcccgggtcgacccacgcgtccg
                                                                                                                                                                                                                                                                                                       10 GGAATTCCCGGGTCGACCCACGCGTCCG
                                                                                                                                                                                                                           ø
                                                                                                 9485613
EST.
                                                                                                                                         T18683
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
                                                                                                                                                        T18683 163 bp n
5C04E02-T7 membrane-free
clone 5C04E02 5' end, mRN
                                                      Zea mays
                                                                                maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gainesville, FL 32611-0
ph: 904-392-1928, ext.
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing Core
University of Florida
P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chris Baysdorfer
Department of Biological Sciences, School of Science
California State University, Hayward
Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helentjaris TG (primary contact)
Dept. of Plant Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interdisciplinary Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Vector: ZipLox; Site_1: SalI; Site_2: NOII; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA PolI. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excisting as plasmids, and then individually analyzed."

[Clone="500605"]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="membrane-free polysomes from endosperm"
/lab_host="DH108"
<1. .>114
33 c 27 g 28 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FL 32611-0695
1928, ext. 301
                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 21;
Pred. No. 1.72e-26;
                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for Biotechnology Research
                                                                                                                                                                                                                                                                                    56
                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                               endosperm
                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                   Zea
                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                               mays
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                  0:
```

```
mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                  RESULT
LOCUS
                                                                                                   Š
                                                                                                                                      g
                  DEFINITION
                                                                                                                                                                        Query Match
Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 163)
Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
Shen,Jaris,T., Baysdorfer,C., Almira,E., Feri,R., Habben,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Mol. Biol. 26, 1085-1101 (1994) 95111093
T18294 184 bp mRNA EST 17-OCT-1996 5c06c10-t7 membrane-free polysomes from endosperm Zea mays cDNA clone 5c06c10 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Partial sequencing and mapping of clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer:
                                                                                                                                                                        6.0%;
Similarity 100.0%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interdisciplinary Center for DNA Sequencing Core University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biological Sciences, School of Science California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dept. of Plant Sciences, University of Arizona, Tucson, AZ, ph: 602-6218-746 fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rob Ferl
                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                           /Strain="W64A2"
/note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
/note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
NotI oligo- dT oligomer and then adding the second strand
to RNase-nicked DNA:RNA hybrid with DNA polI. SalI
adaptors were added to the ends, the ds-cDNAs were then
digested with NotI and size-selected. These were
directionally-cloned into the ZipLox phage vector, excised
as plasmids, and then individually analyzed."
/clone="504E02"
/clone="504E02"
                                                                                                                                                                                                                                                                                            /clone_lib="membrane-free polysomes/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Zea mays"
                                                                                                                                                                                                                                                             .>163
23 c
                                                                                                                                                                      Score 28;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                               27
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biotechnology Research
                                                                                                                                                                                            DB 21;
1.72e-26;
                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                               ct
                                                                                                                                                                                                           Length 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from two maize cDNA
                                                                                                                                                                                                                                                                 IJ
                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                    from endosperm"
                                                                                                                                                                            0
                                                                                                                                                                            Gaps
                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIN
   밁
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                         source
   10 GGAATTCCCGGGTCGACCCACGCGTCCG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T18294
g463327
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carkins, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing Core
University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: T7
                                                                                                                           42 a
```

```
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Lillopsida; Poales; Poaceae; Zea.
1 (bases 1 to 184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T. Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences, School of California State University, Hayward Hayward, CA 94542
ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interdisciplinary Center for Biotechnology Research
                                                                                                                                                                                                                                                                                /note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cpnn was prepared from oilgo-dT selected mRNA by prinning with a notI oilgo-dT oilgomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA PolI. SalI adaptors were added to the ends, the ds-cDNAs were them digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, exciscular plasmids, and then individually analyzed."

/clone="5c06c10"
                                                                                                                                                             /clone_lib-"membrane-free polysomes from endosperm"
/lab_host="DH10B"
<l. .>184
38 c 42 g 61 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26, 1085-1101 (1994)
Score 28; DB 21;
Pred. No. 1.72e-26;
0; Mismatches 0
                                                                     Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCreery, T.,
```

0;

Gaps

0

ö

Gaps

ö

```
Direct Submission
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm,
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 340)
Gress, T.M., Muller-Pillasch, F., Geng, M., Zimmerhacki, F., Zehfetner, G., Friess, H., Buchler, M., Adler, G. and Lehrach, H. A pancreatic cancer-specific expression profile oncogene 13 (8), 1819-1830 (1996)
                                                                                                                                                                                                                                                                                      13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 350)
Gress, T.M., Muller-Pillasch, F., Geng, M., Zimmerhackl, F., Zehetner, G., Friess, H., Buchler, M., Adler, G. and Lehrach, H. A pancreatic cancer-specific expression profile oncogene 13 (8), 1819-1830 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 340)
Mueller-Pillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 350)
Mueller-Pillasch, F., Zimmerhackl, F., Geng, M. and Gress, T.M.
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/note="overexpressed in pancreatic cancer"
/db_xref="taxon:9606"
/cell_line="Patu 8988t"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
                                  others
                                                                                       Length 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 others
                                                                                     re 28; DB 21; Length 221
1. No. 1.72e-26;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 23; Length 340
Pred. No. 1.72e-26;
0; Mismatches 0; Indels
                                17
                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pancreatic cancer"
/clone="xs359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 t
                              25
                                                                                                                                                                                                                                                                                 HSU46345 340 bp mRNA
Human clone xs359 mRNA sequence.
U46545
91236487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSU46346 350 bp MRNA Human clone xs360 mRNA sequence.
                                                                                       Score 28;
Pred. No.
                                                                                                                                                                31 GGAATTCCCGGGTCGACCCACGCGTCCG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         649
                                ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 ggaatteeegggtegaeeeaegegteeg
                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
          <1. .>221
1 66 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                            47 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91236488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                     uman.
mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                 RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                        ò
                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: ZipLox; Site_1: Sal1; Site_2: Not1; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a Not1 oligo-dT oligo-dT notigned man then adding the second strand to RNASe-nicked DNA: RNA hybrid with DNA Pol1. Sal1 adaptors were added to the ends, the ds-cDNAs were then digested with Not1 and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

/db xref="taxon:457"
/clone="5CotFO2"
/clone="15CotFO2"
/clone=lib="membrane-free polysomes from endosperm"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 221)
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                     T18691 221 bp mRNA EST 17-OCT-1996 5C04F02-T7 membrane-free polysomes from endosperm Zea mays CDNA clone 5C04F02 S' end similar to 17.5 KD Class II heat shock protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences, School of Science California State University, Hayward, CA 94542
Hayward, CA 94542
ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interdisciplinary Center for Biotechnology Research May Sequencing Core University of Florida P.O. Bo. 2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contact)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: The Maize cDNA Project
      /organism="2ea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helentjaris TG (primary
Dept. of Plant Sciences
University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: I7
                                                                                                                                                                                                                                                                                                                                                                                                     Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ibraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rob Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95111093
                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                           maize.
                                                                                   RESULT 11
                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
COMMENT
                          59
                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
```

ö

Gaps

œ

```
Search completed: Mon Mar 8 23:35:10 1999
                                                                                                   Larkins, B
                                                                                                                                    libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rob Ferl
                                                                                                                                                                      95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
BASE COUNT
                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                     REFERENCE
                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                     TITLE
                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T18713 386 bp mRNA EST 17-0CT-1996 5C04G09-T7 membrane-free polysomes from endosperm Zea mays CDNA clone 5C04G09 5' end similar to 40s ribosomal protein S8, mRNA
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm, Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany Location/Qualifiers
1. .350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 360)
Mueller-Pillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.
Direct Submission
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm,
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryotee; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
Gress, T.M., Muller-Pillasch, F., Geng, M., Zimmerhackl, F.,
Zehetner, G., Friess, H., Buchler, M., Adler, G. and Lehrach, H.
A pancreatic cancer-specific expression profile
Oncogene 13 (8), 1819-1830 (1996)
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 23; Length 360;
Pred. No. 1.72e-26;
0; Mismatches 0; Indels
                                                                                                                                                                                                                Score 28; DB 23; Length 350;
Pred. No. 1.72e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="overexpressed in pancreatic cancer"
/db_xref="taxon:9606"
                                                                                       cancer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 others
                                                                                                                                                                      11 others
                                                                                                                                                                                                                                                  0; Indels
                                                                 /organism="Homo sapiens"
/note="overexpressed in pancreatic
/db.xref="taxon:9606"
/cell_line="ratu 8988t"
/tissue_type="pancreatic cancer"
/clone="xs360"
                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pancreatic cancer"/clone="xs366"
                                                                                                                                                                   99 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 t
                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_line="Patu 8988t"
                                                                                                                                                                                                                                                                                                                                                          Human clone xs366 mRNA sequence. U46350 gg1336492
                                                                                                                                                                                                                                                                                   34 GGAATTCCCGGGTCGACCCACGCGTCCG 61
                                                                                                                                                                                                                                                                                                  29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 GGAATTCCCGGGTCGACCCACGCGTCCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 g
                                                                                                                                                                    77 g
                                                                                                                                                                                                                  Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
T18713
9485643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maize.
Zea mays
                                                                                                                                                                   104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                       source
                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

)

J

```
/note="Vector: ZipLox; Site_1: Sali; Site_2: Not!; ds-cDNA was prepared from oligo-dr selected mRNA by priming with a Not! oligo-dr oligo-dr selected mRNA by priming with a to RNase-nicked DNA: RNA hybrid with DNA Pol!. Sali adaptors were added to the ends, the ds-cDNAs were then digested with Not! and slae-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

/clone="5C4G409"
/clone="5C4G09"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                             Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85723
ph. 602-6218-746
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Lillopsida; Poales; Poaceae; Zea.
1 (bases 1 to 386)
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                            Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biological Sciences, School of Science California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interdisciplinary Center for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 21; Le
Pred. No. 1.72e-26;
0; Mismatches 0;
                                                                                                                                                                                                                              Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fax: 602-621-7186
E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                       Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .386
/organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GGAATTCCCGGGTCGACCCACGCGTCCG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing Core
University of Florida
P.O. Box 100695
Gainesville, FL 32611-0695
ph: 904-392-1228, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%;
Local Similarity 100.0%;
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .>386
92 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayward, CA 94542
ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: T7
```

Job time : 1491 secs.

US-09-206-040-1.rst

CLEEN AND THE STATE OF THE STAT

•

-

	(TM)
'	
'	
	7/2/
<u></u>	
 	- -
 \	
	}
	<u></u>

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Mon Mar 8 22:14:44 1999; MasPar time 35.64 Seconds 1138.185 Million cell updates/sec Run on:

not generated. Tabular output >US-09-206-040-1 (1-469) from US09206040A.seq 465 Description: Perfect Score: N.A. Sequence:

1 ttaacttgcagcgnccaggt........gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.......ctactatgtaacttctanna

Scoring table:

TABLE default Gap 6

165359 seqs, 43243793 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 7.884; Variance 3.978; scale 1.982

Statistics:

SUMMARIES

		æ						
Result No.	Score	Ouery Match	Query Match Length DB	DB	DI DI	Description		Pred. No.
-	45	9.7	7218	2	US-08-232-	Sequence 14, Applicati	Applicati	5.20e-17
7	40	9.8	1023	m	US-08-785-	Seguence 2, A	Applicatio	1.91e-13
Э	38	8.2	570	m	US-08-633-	-	Applicatio	4.81e-12
4	38	8.5	696	m	us-08-700-	٠ ,	Applicatio	4.81e-12
Ŋ	38	8.2	1529	ო	US-08-726-	٦,	Applicatio	4.81e-12
ø	38	8.2	1581	m	US-08-460-	1,	Applicatio	4.81e-12
7	38	8.2	1581	~	US-08-383-	7	Applicatio	4.81e-12
ω	37	8.0	965	m	US-08-388-	22,	Applicati	2.38e-11
σ	36	7.7	7218	~	US-08-232-	14,	Applicati	1.16e-10
10	29	6.2	215	-	US-08-238-	'n	Applicatio	5.54e-06
11	27	5.8	215	-	US-08-238-	Š	Applicatio	1.05e-04
12	27	5.8	538	m	-068-80-SD	-	Applicatio	1.05e-04
13	27	5.8	2606	m	us-08-568-	7	, Applicatio	1.05e-04
14	26	5.6	965	m	US-08-388-	7	Applicati	4.45e-04
15	25	5.4	74	4	PCT-US95-1	Sequence 94,	Applicati	1.85e-03
16	25	5.4	81	4	PCT-US95-1	92,	Applicati	1.85e-03
17	24	5.2	74	4	PCT-US95-1	100,	Applicat	7.50e-03
18	24	5.2	81	4	PCT-US95-1	98,	Applicati	7.50e-03
13	23	4.9	75	4	PCT-US95-1	Sequence 99,	Applicati	2.97e-02
20	23	4.9	82	4	PCT-US95-1		Applicati	2.97e-02
							:	

· ·	
1.15e-01 1.1	1.57e+00
Sequence 100, Applicati Sequence 99, Applicati Sequence 97, Applicati Sequence 97, Applicati Sequence 16, Applicati Sequence 14, Applicati Sequence 145, Applicati Sequence 145, Applicati Sequence 147, Applicati Sequence 147, Applicati Sequence 14, Applicati Sequence 11, Applicati Sequence 11, Applicati Sequence 11, Applicati Sequence 11, Applicatio Sequence 11, Applicatio Sequence 12, Applicatio Sequence 13, Applicatio Sequence 14, Applicatio Sequence 14, Applicatio Sequence 14, Applicatio Sequence 14, Applicatio Sequence 14, Applicatio Sequence 13, Applicatio	'n
PCT-US95-1 Seq PCT-US95-1 Seq PCT-US95-1 Seq PCT-US95-1 Seq US-08-353- Seq US-08-452- Seq US-08-471- Seq	
PCG4 PCG4 PCG4 PCG4 PCG4 PCG4 PCG4 PCG4	4 PCT
74 75 75 75 75 75 75 75 75 75 75 75 75 75	24979
22222221111111111111111111111111111111	6.4.3
	5 20
0 00 00000 0	4

ALIGNMENTS

COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDTUM TYPE: FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA FLIASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)836-9300
TELEFAX: (703)836-9300 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: RESULT

linear

```
16 caggtancggtcaggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 86
            TOPOLOGY: 11ne
IMMEDIATE SOURCE:
   STRANDEDNESS:
                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                         XXXXXX
                                                                                              Matches
                                                                                                                                                                   RESULT
                                                                                                                   셤
   888888
                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                          150 ctttgctttgcatctatcgaattctaatccaattctctctgcatctacatatacaatatc 209
                                                                                                                                                                             210 ataatcgttcataagattgcatttgcattgatttcaaaaatgcagatcaggggatcgagt 269
                                                                                                                                                                                                                       270 cacagactctccagtatgggcaataatcgatcccgcattcccgcgctcctcatctccatg 329
                                                                                                        Gaps
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08785065
SEPPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                   CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                 Query Match 9.7%; Score 45; DB 2; Length 7218; Best Local Similarity 0.5%; Pred. No. 5.20e-17; Matches 1; Conservative 127; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/785,065 FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                    .r 2
US-08-785-065-2 STANDARD; DNA; UNC; 1023 BP
                                                                                                                                                                                                                                                 1405 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0187 US
                                                                                                                                                                                                                                                              330 ttcgccactttcgcttctatctacgtcgctg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFLING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1023 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                               TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Port
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                  88888888
                                                                                                                                                                                       δ
                                                                                                                                                                                                        a
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ċ
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                  ö
                                                                                                                                81
                                                                                                                                                                                                                                                                    / Match 8.6%; Score 40; DB 3; Length 1023; Local Similarity 86.5%; Pred. No. 1.91e-13; nes 45; Conservative 0; Mismatches 7; Indels
                                                                                                                                                 30 CIGGIAGCCIGCAGGIACCGGICCGGAATICCCGGGICGACCCACGCGICCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%; Score 38; DB 3; Length 570; 55.1%; Pred. No. 4.81e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
LIBRARY: Consensus
CLONE: Consensus
SEQUENCE 1023 BP; 217 A; 270 C; 290 G; 246 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: 836820
SEQUENCE 570 BP; 149 A; 155 C; 137 G; 129 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                    STREE: 3174 Porter Drive CITY: Palo Alto COUNTY: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTAMES: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,682
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0063 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                            .r 3
US-08-633-682-1 STANDARD; DNA; UNC; 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 570 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY:
```

XXXXXX

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08460898
Sequence 1, Application US/08460898
Sequence 1, Application US/08460898
Sequence 1, Application US/08460898
CGENERAL INFORMATION:
APPLICANT: Debesh, Katayoon
APPLICANT: Debesh, Ratayoon
APPLICANT: Davies, Huw Maelor
TITLE OF INVENTION: Production of Myristate in Plant Cells
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STREET: 1920 Fifth Street
CITY: Davis
CONTINE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER: Apple Macintosh 7.0
COMPUTER: Apple Macintosh 7.0
COMPUTER: Apple Macintosh 7.0
CORPATARE: Microsoft Word 5.1(a)
CORPATARE: Microsoft Word 5.1(a)
CORPATARE: US-0408-1995
CHILING DATE: 05-0408-1995
CLASSIFICATION DATA:
APPLICATION UNMBER: 08/383,756
FILING DATE: 02-185-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                 COMPUTER READABLE FORM:
MEDIUM TYPE: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: LBM 466
COMPUTER: WINDER: US/08/726,575A
FILICATION NUMBER: US/08/726,575A
FILICATION NUMBER: US/08/726,575A
FILICATION NUMBER: 34,344
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: ATTORNEY AGENT INFORMATION:
NAME: William T Han 34,344
REFERENCE/COCKET NUMBER: 34,344
REFERENCE/COCKET NUMBER: TELEPHONE: 610 270 4026
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1529 BP; 390 A; 374 C; 315 G; 450 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 3; LA
Pred. No. 4.81e-12;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UT 6
US-08-460-898-1 STANDARD; DNA; UNC; 1581 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.2%;
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
  2222222222222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08726575A
Sequence 1, Application US/08726575A
Sequence 1, Application US/08726575A
Sequence 1, Application US/08726575A
Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 2, Sequence 3, Se
                                                          Sequence 1, Application US/08700637
Sequence 1, Application US/08700637
Sequence 1, Application US/08700637
Patent No. 5654413
GENERAL INFORMATION:
APPLICANT: Hawkins, Phillip R.
APPLICANT: Stuart, Susan G.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON NUMBER OF SEQUENCES: 12
CORRESPONDENCES. 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STRRET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 3; Length 969;
Pred. No. 4.81e-12;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: COLNNOT05
CLONE: 775426
SEQUENCE 969 BP; 163 A; 324 C; 280 G; 202 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .r 5
US-08-726-575A-1 STANDARD; DNA; UNC; 1529 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKette
COMPUTER: DEM COMPATIBLE
COMPUTER: DEM COMPATIBLE
COMPUTER: DEM COMPATIBLE
SOFTWARE: FESTESQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700, 637
FILING DATE: FILEG HEEWAITH
ATTORNEY, AGENT INFORMATION:
NAME: LUTHER, BALDARA J.
RECISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0065 US
TELEPHONE: 415-852-0555
TELEPHONE: 415-852-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 bairs
US-08-700-637-1 STANDARD; DNA; UNC; 969 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.2%;
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
```

XXXXXX

RESULT

셤

ò

```
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5795961man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       XXXXX
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                 g
    888888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08383756
Sequence 1, Application US/08383756
Sequence 1, Application US/08383756
Sequence 1, Application US/08383756
C Patent No. 5654495
C GENERAL INFORMATION:
APPLICANT: Debesh, Katayoon
APPLICANT: Debesh, Toni Alois
APPLICANT: Devises, Huw Maelor
TITLE OF INVENTION: Production of Myristate in Plant Cells
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                     Length 1581;
                                                                                                                                                                                                                                                                                                                     Query Match 8.2%; Score 38; DB 3; Length 1581
Best Local Similarity 95.1%; Pred. No. 4.81e-12;
Matches 39; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
SEQUENCE 1581 BP: 418 A; 356 C; 410 G; 397 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,695
FILING DATE: 16-JUN-94
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29-OCT-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 07/968,971
FILING DATE: 30-OCT-92
ATTORNEY, AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna B: Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J: Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: 36,924
REFERENCE/DOCKET NUMBER: GIS)
TELECAMUNICATION INPORMATION:
TELECAMUNICATION INPORMATION:
TELECAMUNICATION INPORMATION:
TELECAM: (916) 753-1510
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1581 base pairs
TYRE. DUCLEIC COURTERING SEO ID NO: 1
LENGTH: 1581 base pairs
TYRE. DUCLEIC COURTERING SEO ID NO: 1
LENGTH: 1581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,756
FILING DATE: 02-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,695
FILING DATE: 16-JUN-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 95616
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
    $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 8.2%; Score 38; DB 2; Length 1581; Local Similarity 95.1%; Pred. No. 4.81e-12; les 39; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08388672A
Sequence 22, Application US/08388672A
Sequence 22, Application US/08388672A
Patent No. 5795561
GENERAL INFORMATION:
APPLICANT: Wallace, T. Paul
APPLICANT: Harris, William J.
APPLICANT: Carr, Frank J.
APPLICANT: Welt, Sydney
APPLICANT: Welt, Sydney
APPLICANT: Witamura, Kunio
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
SEQUENCE 1581 BP; 418 A; 356 C; 410 G; 397 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/388,672A
FILING DATE: 14-FEB-1995
TTORNEY APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 caggtancggtcaggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 CAGGTACCGGTCCGGGAATTCCCGGGTCGACCCACGCGTCCG 81
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10814
FILING DATE: 29-OCT-93
CLASSIFICATION ATS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/968,971
FILING DATE: 30-OCT-92
ATTORNEY/AGENT INFORMATION:
NAME: Blizabeth Lassen
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKT NUMBER: 36,924
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 8
US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Felfe and Lynch
STREET: 805 Third Avenue
CITY: New YORK
STATE: New YORK
COUNTRY: U.S.A.
```

ë

;

```
XXXXXX
                                                                                              Matches
                                                                                                                                                                                                                                      RESULT
       ឧឧឧ
                                                                                                                                                                      셤
                                                                                                                                                                                                გ
                                                                                                                                                                                                                       784 HUVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTMADTSSNSR 843
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                 ä
REFERENCE/DOCKET NUMBER: LUD 5409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-9200
TELEFAX: 212-838-984
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH 965 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                       324 agatgaggagggggaatgcggggatcgattattgcccatactggagag 276
                                                                                                                                                                                                                                                                        844 SSVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHUVKDMTSSSSAS 892
                                                                                                                                                                    Query Match 8.0%; Score 37; DB 3; Length 965; Best Local Similarity 19.3%; Pred. No. 2.38e-11; Matches 21; Conservative 53; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5570367
GENERAL INFORMATION:
APPLICANT: CORNET CORNET. FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)883-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE: 26-AUC-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUC-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                     .T 9
US-08-232-463-14 STANDARD; DNA; UNC; 7218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                    පු
      88888888888888
                                                                                                                                                                                                                                               S
```

```
Sequence 5, Application US/08238163
C SEGREAL INFORMATION:
C APPLICANT: BENNETT, Alan
C APPLICANT: LABATTCH, John M.
APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
CORRESPONDENCE ADDRESS:
CC CRESPONDENCE ADDRESS:
CC CRESPONDENCE ADDRESS:
CC CTRY: San Francisc
CC CITY: San Francisc
CC COUNTRY: US
CC COUNTRY: US
CC CLIP: 94105-1493
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                       149 tetttggtgetgetgetactttttetggteaagaaagteaceaagaateceetett 90
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of FGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pT2gpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                               Score 36; DB 2; Length 7218;
Pred. No. 1.16e-10;
61; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 1; Length 215;
Pred. No. 5.54e-06;
65; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                             1405 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTAC 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORKEY AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTATION NUMBER: 34,774
REPERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 543-9600
TELEFAX: (415) 543-543
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                       JT 10
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                               7.7%;
Similarity 4.3%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 12.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
```

```
ö
90 DSKTVTDSYNASGISSSNGGTDGNRSGADSYGSSKTAMIS-RNRIGKIANNAVDSRNMGD 148
                       242 aatcaatgcaaatgcaatcttatgaacgattatgatattgtatatgtagatgcagagaga 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                         149 ASVGSDKNTKKHAKNSADGKV-GSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVS 202
                                                                                                                 ö
                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08890572
GENERAL INFORMATION:
APPLICANT: PLATICA ET AL.
TITLE OF INVENTION: PITUITARY DIFFERENTIATION
TITLE OF INVENTION: FACTOR AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Pituitary Differentiation Factor SEQUENCE 538 BP; 129 A; 123 C; 137 G; 141 T; 8 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 3; Length 538;
Pred. No. 1.05e-04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DARA:
APPLICATION NUMBER: USSN 60/021,589
FILING DATE: July 11, 1996
ATORNEY AGENT INFORMATION:
NAME: Clark, Richard S
RECISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: AP30487 165/33281
TELECOMMUNICATION:
TELECHONE: 212-408-2558
TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brumbaugh, Graves, Donohue
ADDRESSEE: Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                      JT 12
US-08-890-572-1 STANDARD; DNA; UNC; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FESTEM: DOS
SOFTWARE: FESTESEQ VEYSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,572
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 caggtancggtcaggaattcccgggtcgac 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 CAGGTACCGGTCCGGAATTCCCGGGTCGAC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.8%;
Best Local Similarity 93.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                         셤
                                                                                                                                      g
                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08238163
Setel No. 55569330
APPLICANT: BENNETT, Alan
APPLICANT: BENNETT, Alan
APPLICANT: BTOTZ, Henrik
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                              302 ggatcgattattgcccatactggagagtctgtgactcgatcccctgatctgcatttttga 243
                       :|:: : :::: |: : :: :: :: :: :: :| 263 atcgatccgagactctccatataggacaataatcgatcccgcacttcccgcgctctcat 322
                                                                                         64 ANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 SSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAKTHYYTHTNVSGA 89
4 VTMSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 27; DB 1; Length 215;
Pred. No. 1.05e-04;
67; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 94105-1493
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MA-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    RESULT 11

11 US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC XXXXXX

DE Sequence 5, Application US/08238163
CC PACENT NO. 556930
CC APPLICANT: DEBNETT, Alan
CC APPLICANT: DEBNETT, Alan
CC APPLICANT: POWELL, Ann
APPLICANT: STOTZ, Henrik
CC TILLE OF INVENTION: PLANT INHIBITORS OF
CC TILLE OF INVENTION: POLYGALACTURONASES
CC CORRESPONDENCE ADDRESS:
CC TILLE OF INVENTION: POLYGALACTURONASES
CC CORRESPONDENCE ADDRESS:
CC CORRESPONDENCE ADDRESS:
CC STREET: Steuart Street Tower, One Mar
CC STREET: Steuart STREET: POOS/NS-DOS
CC CONNTRY: US
CC COMPUTER: IBM PC COMPATA:
CC COMPUTER: IBM PC COMPATA:
CC CORPERATING SYSTEM: PC-DOS/NS-DOS
CC CORPERATING SYSTEM: PC-DOS/NS-DOS
CC CATCORNEY. SEETING NOWNER: 230.163
CC CATCORNEY. SEETING NOWNER: 230.00
CC C CATCORNEY. SEETING NOWNER: 230.00
CC C CATCORNEY. SEETING NOWNER: 230.00
CC C CONTRENT NOWNER: 230.00
CC CONTRENT NOWNER: 230.00
CC C CONTRENT NOWNER: 230.00
CC C CONTREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                   124 KTAMTSRNRTGKTANNAVDSRNMGDASVGSDK 155
                                                                                                                                                                                                                           383 g-aatcgcgtttatctcatcaaagagctcgat 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.8%;
Best Local Similarity 14.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
a
                                                                                                                                    à
                                                                                                                                                                              g
```

```
810 WVRGRGWGDYGGGYTNYNGKRGRVTMADTSSNSRSSVTAADTAVYYCVRGRSYDSDGGDY 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870 WGGTIVIVSSHUVKDMISSSSASVGDRVITCRSSTIHGNGNIYYWYKGKAKYRVSNRSGV 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.6%; Score 26; DB 3; Length 965; Best Local Similarity 15.8%; Pred. No. 4.45e-04; Matches 22; Conservative 60; Mismatches 56; Indels
                                                                                                                                 COUNTRY: New YORK
COUNTRY: U.S.A.

ZIT: New YORK
COUNTRY: U.S.A.

ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,672A
FILING DATE: 14-FEB-1995
CLASSIFICATION:
NAME: HABSON, NO. 5795961man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 1.UD 5409
TELEPHONE: 212-888-9200
TELEPHONE: 212-888-9300
TELEPHONE: 212-838-3844
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 965 base pairs
TYPE: NULLEIC CALL
STRANDEDNESS: UNKNOWN
STRANDEDNESS: UNKNOWN
APPLICANT: Old, Lloyd J.
APPLICANT: Welt, Sydney
APPLICANT: Kitamura, Kunio
TITLE OF INVENTION: Recombinant Human Anti-Lewis B
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe and Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .T 15
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   930 SRSGSGSGTDYTTSSDATY 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 gacgcagagaatcgcgttt 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                    APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Allier, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wallems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASWODIUW VIVAX
TITLE OF INVENTION: AND PLASWODIUM FALCIPARUM ERTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 3; Length 2606;
Pred. No. 1.05e-04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                          COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen. Ned
REGISTRATION: NUMBER: 29,655
REFERENCE/DOCKET NUMBER: WIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2606 base pairs
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Plasmodium falciparum
SEQUENCE 2606 BP; 992 A; 351 C; 569 G; 694 T; 0 OTHER.
            JT 13
US-08-568-459A-7 STANDARD; DNA; UNC; 2606 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .T 14
US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08388672A Sequence 22, Application US/08388672A Patent No. 5795961 GENERAL INFORMATION:
APPLICANT: Wallace, T. Paul APPLICANT: Harris, William J. APPLICANT: Carr, Frank J.
                                                                  Sequence 7, Application US/08568459A Sequence 7, Application US/08568459A Patent No. 5849306 PEREMAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.8%;
Best Local Similarity 93.3%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

1; Gaps

```
CC COMPUTER READABLE FORM:
CC COMPUTER READABLE FORM:
CC COMPUTER: IBM PC compatible
CC COMPUTER: IBM PC compatible
CC COMPUTER: IBM PC compatible
CC CURRENT APPLICATION DATA:
CC CURRENT APPLICATION NUMBER: PCT/US95/11934
CC CURRENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC ATTORNEY/AGENT INFORMATION:
CC TELECHONE: (212) 790-9090
CC TELECHONIC: (212) 790-9090
CC TELECHONIC: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEFAX: (212) 869-9741/8864
CC TELEFAX: (212) 869-9741/8864
CC TELEFAX: (212) 869-9741/8864
CC TELEFAX: (213) 789-9090
CC TELEFAX: (213) 789-9090
CC TELEFAX: (213) 789-9090
CC TELEFAX: (213) 789-9091
CC SEQUENCE CHARACTERISTICS:
CC TOPOLOGY: linear
CC SEQUENCE TYPE: DNA (genomic)
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC TOPOLOGY: linear
CC TOPOLOGY: linear
CC TOPOLOGY: linear
CC SEQUENCE TYPE: DNA (genomic)
CC SEQUENCE TY BP: 3 A; 4 C; 3 G; 1 T; 63 OTHER.
CC TOPOLOGY: linear
CC SEQUENCE TY BP: 3 A; 4 C; 3 G; 1 T; 63 OTHER.
CC SEQUENCE TY BP: 3 A; 4 C; 3 G; 1 T; 63 OTHER.
CC TOPOLOGY: linear
CC SEQUENCE TY BP: 3 A; 4 C; 3 G; 1 T; 63 OTHER.
CC SEQUENCE TY BP: MATCHOS 18; Mismatches 45; Indels 0; Gaps 0;
MATCHOS 10; CONSERVATIVE 18; MISMATCHES 45; Indels 0;
```

Oy 324 tccatgttcgcca 336
Search completed: Mon Mar 8 22:16:44 1999
Job time: 120 secs.

61 NNBNNBNACGCCA 73

97 Pp 93

```
(ME)
```

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

Mon Mar 8 21:44:20 1999; MasPar time 628.63 Seconds 1336.036 Million cell updates/sec Tabular output not generated. Run on:

1 ttaacttgcagcgnccaggt.......qatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.......ctactatgtaacttctanna >US-09-206-040-1 (1-469) from US09206040A.seq 465 Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 .. Nmatch STD

2275026 seqs, 895388244 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est56 Database:

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est109 sgb_est1 6:qb_est10 7:qb_est11 8:qb_est12 9:qb_est13 10:qb_est14 11:qb_est15 12:qb_est16 13:qb_est17 14:qb_est18 15:qb_est19 16:qb_est2 17:qb_est20 18:qb_est21 19:qb_est3 20:qb_est4 21:qb_est5 22:qb_est6 23:qb_est7 24:qb_est8 25:qb_est9 26:qb_gss1 27:qb_gss2 28:qb_gss3 29:qb_gss4 Database:

Mean 10.263; Variance 1.889; scale 5.433 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Pred. No.	4.58e-113	1.43e-74	3.86e-55	1.35e-47	4.80e-42	4.95e-33	4.95e-33	2.86e-31	2.86e-31	2.86e-31	2.86e-31	2.86e-31	1.59e-29
		Description	Rice cDNA, partial sed	97SN1787 Rice Immature	97SN1787 Rice Immature	97SN1784 Rice Immature	97SN1784 Rice Immature	5C04C06-T7 membrane-fr	5C04F08-T7 membrane-fr	Human clone xs368 mRNA	5C04E09-T7 membrane-fr	05c04d02-t7 membrane-f	Homo sapiens mRNA; exp	5C02H01-T7 membrane-fr	5C04E02-T7 membrane-fr
SUMMARIES		ID	C74877	AA754459	AA754459	AA754458	AA754458	T18678	T18698	HSU46351	T18686	T14703	96£66ZSH	T18668	T18683
		DB	. 6	12	12	12	12	21	21	23	21	21	σ	21	21
		datch Length DB	462	252	252	247	247	468	568	390	436	583	589	699	163
ď	Query	Match	17.4	13.3	11.2	10.3	7.6	8.6	8.6	8.4	8.4	8.4	8.4	8.4	8.2
		Score	81	62	52	48	45	40	40	39	39	39	39	39	38
	Result	NO.	-	7	е С	4	C 5	φ	7	80	σ	10	c 11	12	13

9e-2	1.59e-29	.59e-2	.59e-2	9e-2	9e-2	9e-2	9e-2	9e-2	e-2	9e-2	9e-2	9e-2	9e-2	e-2	9e-2	9e-2	9e-2	9e-2	9e-2	9e-2	ç	9e-2	9e-2	9e-2	9e-2	e-2	9e-2	9e-2	.59e-2	9e-2	9e-2
Human clone xs366 mRNA	05c03g08-f21 membrane-	uman clone xs361 mR	5C04F05-T7 membrane-fr	5C04B01-T7 membrane-fr	05c04h07-f21 membrane-	T7 men	clone	5C02G02-T7 membrane-fr	-T7	5C04F10-T7 membrane-fr	17 m	lone xs353 mR	5c06c07-t7 membrane-fr	5C04A03-T7 membrane-fr	-T7	5-T7	5C04F09-T7 membrane-fr	C04G07-T7	5c06c11-t7 membrane-fr	·t7	5C04G03-T7 membrane-fr	5C04E08-T7 membrane-fr	5C04E07-T7 membrane-fr	-T7	5C04F06-T7 membrane-fr	is radiata som	DM00L51		human em	3 human	_
046	14653	046	369	9	174	72	046	98	T18701	87	0	J46	329	67	370	872	869	T18709	829	828	T18704	868	868	872	T18696	9	1213	2087	13	421	AI142134
~	4 21	~	N	~	~	~	N	~	~	~	~	~	~	~	4	7	~	~	ď	~	(1)	0	N	7	~	~	7	~	7	٦	-
9	36	7	^	1	^	σ	0	0	Н	41	-	m	43	n	43	m	43	4	45	S	S	S	S	ø	S	S	1	4	-	88	σ
	8.5	٠	•	•	•	•	٠	•	•	٠			•	٠		•	•	٠	٠			٠		٠	•	•		٠		8.2	•
	38																														
14	c 15	16	17	18	c 19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

C74877 462 bp mRNA EST 18-SEP-1997 (C74877 tece cDNA, partial sequence (E60595_1A), mRNA sequence. (C74877 (C74877 (C7487106 EST; EST(expressed sequence tag). (C792a sativa (strain:Nipponbare) immature leaf including apical meristem (under short day condition) cDNA to mRNA. (STYAB SATIVA EBUKATYOtae; Viridiplantae; Charophyta/Embryophyta group; Eukaryotae; Viridiplants; seed plants; Magnoliophyta; 11,1000, 2000 (C7000)	Sasaki, T. and Yamamoto, K. Sasaki, T. and Yamamoto, K. Nice CDNA from immature leaf including apical meristem Note CDNA from immature leaf including apical meristem (1997) 2 (bases 1 to 462) Sasaki, T. Sasaki, T. Submitted (13-AdG-1997) to the DDBJ/EMBL/GenBank databases. Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program. Rannondal 2-1-2, Tsukuba, Ibaraki 305, Japan (E-mail:tsasak/eabr.affrc.go.jp, Tel:0298-38-7441,	NGP'. Location/Qualifiers 1462 /organism="Oryza sativa" /organism="Oryza sativa" /db_xref="Napponbare" /db_xref="Laxon:4530" /dev_stage="immature leaf including apical meristem (undo::short day condition)" 103 c 145 g 93 t 4 others
EST 60595_1A), mRNA 9). e) immature leaf ition) cDNA to n rophyta/Embryop) seed plants; Mac	ncluding apical ncluding apical bbb/EMBL/GenBayrological i 1-2, Tsukuba, II p, Tel:0298-38-7	va" leaf including & 93 t 4 ot
462 bp mRNA Tial sequence (E) Ssed sequence tack Strain:Nipponbar r short day cond. Tidiplantae; Char ascular plants; sascular	mamoto,K. mamoto,K. following a filter of institute of in	/ RGP'. Location/Qualifiers 1462 /organism="Oryza sativa" /strain="Nipponbare" /db_xref="taxon:4530" /dev_stage="immature lea short day condition)" 103 c 145 g 9
C74877 462 bp mRNA EST 18-SEP- Rice CDNA, partial sequence (E60595_1A), mRNA sequence. C74877 92443106 EST; EST(expressed sequence tag). Oryza sativa (strain:Nipponbare) immature leaf including maristem (under short day condition) cDNA to mRNA. Oryza sativa Eukaryotae; Viridiplantae; Charophyta/Embryophyta group: Embryophyta, vascular plants; seed plants; Magnoliophyta;	Sasaki, T. and Yamamoto, K. Sasaki, T. and Yamamoto, K. Rice cDNA from immature leaf including apical meristem fluctor immature leaf including apical meristem fluctor immature leaf including apical meristem casaki, T. Sasaki, T. Submitted (13-AUG-1997) to the DDBJ/EMBL/GenBank datab. Sasaki, National Institute of Agrobiological Resources Research Program; Rannondai 2-1-2, Tsukuba, Ibaraki 30 (E-mail:tsasaki@abr.affrc.go.jp, Tel:0298-38-7441, Exx.0298-38-7468)	PROJECT - RGP'. Location/(1462 462 / strain="y" / db_xref="//dev_stage" / dev_stage" / dev_stage / de
RESULT 1 LOCUS DEFINITION R ACCESSION 9 KEYWORDS E SOURCE C	CE AL RS AL	COMMENT FEATURES SOURCE SOURCE BASE COUNT

Score 81; DB 9; Length 462; Pred. No. 4.58e-113; 17.4%; 72.9%; Query Match Best Local Similarity US-09-206-040-1.rst

```
141 gctgcggttgctactttct 122
                                                                                                                                                                                                                                                                                                  rice.
                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                            m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                            RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                        ò
                                                        8
                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xho1; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon: 4530"
/clone="97SNI787"
/clone="97SNI787"
/clone="type="Immature Seed Lambda ZAPII cDNA Library"
/fissue_type="Immature Seed"
/dev_stage="5" days after pollination"
/lab_host="E. coli SOLR"
a 21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                              AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
AA754459 92801165
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa Bukaryotae; Charophyta/Embryophyta group; Eukaryotae; Viridiplantae; Charophyta/Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Lilliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 252)

1 (bases 1 to 252)

1 (bases 1 to 252)

Kim, W.T., Kim, W.Y., Zang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Cytogenetics
Mational Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Tes: 82 331 290 0307
Email: myeun&sunZo.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongil, Korea. 449-728 bhnahm@bioserver.myongji.seq primer: M13 Reverse Primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                            89 VGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNTK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : :| | ::::: ::|::::: ::: ::: ::: ::: |:||||: :::: 275 actctccagtatgggcaataatcgatcccgcattcccgcgctcctcatctccatgttcgc 334
                                        TCGCGANTGTCCGCCATGATGCTCGCCATGTTCGCCACCATGGCCTCCTTCTACGTCGCC 109
                                                                                                                   110 GGCCGTCTGTGGCAGGATGCGCAGAGTAGGGTTTACCTGATTAAAGAGCTCGACAGGCGA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 cgttcataagattgcatttgcattgatttcaaaaatgcagatcaggggatcgagtcacag 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTASGWHISINYDVKSSINIW-GVTBSYDKSMHGYWCSBBVKYHIKVSTIRAIRSYICVR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 BVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTKVD 88
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
  ö
                                                                                                                                                                                                 170 ACCGCCCAGGCCCATTCGACGATATCGGTGGATGATACCTTGAAGGTTGT 219
                                                                                                                                                                                                                     Query Match 13.3%; Score 62; DB 12; Length 252; Best Local Similarity 9.9%; Pred. No. 1.43e-74; Matches 22; Conservative 115; Mismatches 85; Indels
  Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 252
/organism="Oryza sativa"
/cultivar="Milyang23"
  .;
o
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Eun M.Y.
  124;
                                                                                                                                                                                                                                                                                                                                                                                                                                      rice.
                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                        20
Matches
                                                                             300
                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                        9
                                                                             ö
                                                                                                               g
                                                                                                                                                      ò
                                                                                                                                                                                               g
                                                                                                                                                                                                                                     ò
```

```
/ Organism="Oryza sativa"
/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note: pBluescript SK(+); Site_1: EcoRI; Site_2:
xhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3'end with Xho I site."
/dLxref="Laxon:4530"
/clone="97SNI787"
/
                                                                                                                                                                                                                                                                                                                                                                                                                           AA754459 252 bp mRNA EST 20-JAN-1998
97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
CDNA clone 97SN1787, mRNA sequence.
AA754459
92801165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 92 bhuatudsun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Seq primer: Ml3 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 DVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRSYTCVRKYCVMWMTKKVVK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 MSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRB 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 aggagcgcgggaatgcggga-tcgattattgcccatactggagagtctgtgactcgatcc 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 VTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNTKCTASGWHTSTNY 160
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Li
Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.2%; Score 52; DB 12; Length 252
Best Local Similarity 9.5%; Pred. No. 3.86e-55;
Matches 19; Conservative 105; Mismatches 74; Indels
                                                                                                                                                                 208 KYCVMWMTKKVVKKYHVVBBGCHBTDSKCKTMWMTNKHVMTST 250
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 KYHVVBBGCHBTDSKCKTMW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Eun M.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
```

LOCUS

RESULT

ACCESSION

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL COMMENT

```
/organism="Oryza sativa"
/organism="Milyang23"
/outlivar="Wallyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII vector at 5 end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                                                                                             Eukaryotae, Viridiplantae, Charophyta/Embryophyta group,
Embryophyta, Tracheophyta, seed plants; Magnoliophyta, Liliopsida;
Poales; Poaceae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="97SN1784"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
Email: myenn@sun20.asti.re.kr
Submitted by Basek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
LOCUS T18678 468 bp mRNA EST 17-OCT-1996
LOCUS 5C04C06-17 membrane-free polysomes from endosperm Zea mays CDNA
Clone 5C04C06 5' end similar to pyruvate phosphate dikinase, mRNA
                                                                                                                                                                                          1 (bases 1 to 247)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                       Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 aatgtatcatcacagata-tagcagattgtccctggccag-tgatcctatcgagctctt 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 RCTNDRGYCNYTA-SDNGT-SATKRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVMV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 gcgaaagtggcgaacatggagatgaggagcggggaatgcgggatcgattattgcccata 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 IBYYSWNVDINTGGTGVGKTIVNVHSGWNNRCSNSVVYVWBIAYCDYBHYBDRANHVDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 WMNKHTHMMTBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKYGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Lillopsida; Poales; Poaceae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.7%; Score 45; DB 12; Length 247; Best Local Similarity 11.4%; Pred. No. 4.80e-42; Matches 24; Conservative 108; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 otl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 ctggagagtctgtgactcgatcccctgatct 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 RITSMWIDKSIKMBSMDMSRRSRVHYGRWMB 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Eun M.Y.
                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
T18678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9485608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maize.
                                                      EST.
rice.
                                                    KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cp
AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
AA754458
92801164
EST.
                                                                                                                                                                                                                                                                                 Oryza sativa

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Magnollophyta; Liliopsida;

Poales; Poaceae; Oryza.

1 (bases 1 to 247)

Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R. Moon,E.P.,

Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,

Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cullival=minyauyaveroript SK(+); Site_1: EcoRI; Site_2:
Xhot; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SNI784"
/clone="97SNI784"
/clone="type="Immature Seed Lambda ZAPII cDNA Library"
/dev_stage="5" advs after pollination"
/lab_host="E. coli SOLR"
a 16 c 21 g 34 t 169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa CDNA clone 97SN1784, mRNA sequence. AA754458 92801164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 GYGTBYYSWNVDINTGGTGVGKTTVNVHSGWNNRCSNSVVYV-WBTAYCDYBHYBDRANH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 BAWMNKHTHMMTBBWCCVRRVGTTTNNGKHNG-RTTTWNDCSDNAHCRYTVBWYYARSKY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 VDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVT-YGSSBYBRCGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.3%; Score 48; DB 12; Length 247; Best Local Similarity 14.6%; Pred. No. 1.35e-47; Matches 31; Conservative 103; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 VMVRTTSMWTDKSTKMBSMDMSRRSRVHYGRW 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gagaatcgcgtttatctcatcaaagagctcga 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"/cultivar="Milyang23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Eun M.Y.
                                                                                                                                                                                                                                                                 rice.
```

source

FEATURES

BASE COUNT

ORIGIN

S

RESULT

381

ò

g

ò

g

요 ò

ò

DEFINITION

ACCESSION NID

ŝ

5; Gaps

78

JOURNAL

COMMENT

TITLE

REFERENCE AUTHORS

```
/note="vector: 2ipLox; Site_1: Sali; Site_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligomer and then adding the second strand to RNAsse-nicked DNA:RNA hybrid with DNA Poli. Sali adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85723
ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
Lillopsida; Poales; Poaceae; Zea.
1 (bases 1 to 568)
Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
                                                                                                                                                                                                                                                                                                       Partial sequencing and mapping of clones from two maize cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chris Baysdorfer
Department of Biological Sciences, School of Science
California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interdisciplinary Center for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 21; Length 568;
Pred. No. 4.95e-33;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing Core
University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.3%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: T7
    mRNA sequence.
F18698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 1
                                                                                                                                                                                                                                                                                 Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rob Ferl
                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                             95111093
                                                9485628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
                                                                                              maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
BASE COUNT
ORIGIN
                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                REFERENCE
AUTHORS
                          ACCESSION
                                             NID
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: ZipLox; Site_1: Sall; Site_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA PolI. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

//clone="5004006"
                                                                                                                                                                                                                                                                               Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                   Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T18698 558 bp mRNA EST 17-OCT-1996 5C04F08-T7 membrane-free polysomes from endosperm Zea mays cDNA clone 5C04F08 5' end similar to 22kd alpha zein alpha precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                 Larkins, B.
Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="membrane-free polysomes from endosperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biological Sciences, School of Science California State University, Hayward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interdisciplinary Center for Biotechnology Research DNA Sequencing Core University of Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 21; Length 468
Pred. No. 4.95e-33;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Mol. Biol. 26, 1085-1101 (1994)
95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.O. Box 100695
Gainesville, FL 32611-0695
pt 904-392-1928, ext. 301
fax: 904-392-4072
E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                fax: 602-621-7186
E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                             Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .468
/organism="Zea mays"
/strain="W64A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%;
Best Local Similarity 89.6%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <1. .>468
(bases 1 to 468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fer]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rob
D
```

source

FEATURES

ö

Gaps

7

RESULT

염 ò

mRNA BASE COUNT ORIGIN

LOCUS DEFINITION

음 ò DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOORNAL MEDLINE REFERENCE

```
/strain="Wedga" "And the property of the prope
      University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85729
ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T14703 583 bp mRNA EST 17-OCT-1996 05c04d02-t7 membrane-free polysomes from endosperm Zea mays cDNA clone 05c04d02 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charophyta/Embryophyta group; Embryophyta; Magnollophyta;
1.11.10psida; Poales; Poaceae; Zea.
1. (bases 1 to 583)
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                         Department of Biological Sciences, School of Science California State University, Hayward Hayward, CA 94542 Ph: 510-811-3459 ph: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rob Ferl
Interdisciplinary Center for Biotechnology Research
DNA Sequencing Core
University of Florida
P.O. Box 100695
gainesville FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 caggtanoggtcaggaattcccgggtcgacccacgcgtccgtac 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 21;
Pred. No. 2.86e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                       E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
<1. .>436
118 c 124 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.4%;
Best Local Similarity 93.2%;
Matches 41; Conservative
                                                                                                  fax: 602-621-7186
                                                                                                                                                                                               Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sed primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRNA
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alondo 436 bp mRNA EST 17-OCT-1996 5C04E09-T7 membrane-free polysomes from endosperm Zea mays CDNA clone SC04E09 5' end similar to glyceraldehyde-3-phosphate dehydrogenase, mRNA sequence. T18686 gq485616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm,
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany
Location/Qualifiers
                                                                                                                                                                                               13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae: mitochondrial eukaryotes: Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 390) Gress, T.W. Muller-Pillasch, F., Geng, M., Zimmerhackl, F., Zehetner, G., Friess, H., Buchler, M., Adler, G. and Lehrach, H. A pancreatic cancer-specific expression profile 00ncogene 13 (8), 1819-1830 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 390)
Mueller-Fillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .390
/organism="Homo sapiens"
/note="overexpressed in pancreatic cancer"
/db_xref="taxon:9606"
/cell_line="Patu 8988t"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCTCGCCAGC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 23; Length 390
Pred. No. 2.86e-31;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pancreatic cancer"
/clone="xs368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    libraries
Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helentjaris TG (primary contact)
Dept. of Plant Sciences
                                                                                                                                                                                        HSU46351 390 bp mRNA
Human clone xs368 mRNA sequence.
U46351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 8.4%;
Best Local Similarity 88.0%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 c
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larkins, B.
                                                                                                                                                                                                                                                                                        91236493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    maize.
```

source

FEATURES

TITLE JOURNAL

AUTHORS

BASE COUNT

ORIGIN

σ

RESULT

셤 ô LOCUS

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

JOURNAL MEDLINE

COMMENT

TITLE

ö

Gaps

JOURNAL MEDLINE COMMENT

```
Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
I (bases I to 669)
Shen. B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T18668 669 bp mRNA EST 17-0CT-1996 5C02H01-T7 membrane-free polysomes from endosperm Zea mays CDNA clone 5C0ZH01 5' end, mRNA sequence. T18668 9485598 EST.
                                                                                          Direct Submission
Submitted (11-SEP-1997) Korn B., Institution Molekulare
Genomanalyse, Deutsches Krebsforschungszentrum Heidelberg, Im
Neuenheimer Feld 506, D-69120 Heidelberg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interdisciplinary Center for Biotechnology Research DNA Sequencing Core University of Florida P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 9; Length 589;
Pred. No. 2.86e-31;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 ACGGACGCGTGGGTCGACCCGGGAATTCCGGACCGGTACCTG 439
    Wiemann, S., Ebert, L. and Poustka, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chris Baysdorfer
Department of Biological Sciences, School
California State University, Hayward
Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                      120 t
                                                                                                                                                                             Location/Qualifiers
1. 589
/organism="Homo sapiens"
/db.ref="taxon:9606"
/clone="tkF2phamy1"
/clone="tkF2phamy1"
/tissue_type="amygdala"
/dev.stage="amygdala"
/dev.stage="amygdala"
/dev.stage="amygdala"
/dev.stage="amygdala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.2%;
Matches 40; Conservative
                                             (bases 1 to 589)
    Korn, B., Wie
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             libraries
                                                                       Korn, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
AUTHORS
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
COMMENT
                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="W64A2" merys
//strain="W64A2" merys
//note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT oligomer and then adding the second strand
to RNase-nicked DNA:RNA hybrid with DNA PolI. SalI
adaptors were added to the ends, the ds-cDNAs were then
digested with NotI and size-selected. These were
directionally-cloned into the ZipLox phage vector, excised
as plasmids, and then individually analyzed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSZ99396 589 bp DNA EST 19-SEP-1997
Homo sapiens mRNA; expressed sequence tag; clone DKFZphamyl_lc11,
                                                                                                                                  Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ,85721
ph: 602-6218-746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="05c04d02"
/clone_lib="membrane-free polysomes from endosperm"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                    Chris Baysdorfer
Department of Biological Sciences, School of Science
California State University, Hayward
Hayward, CA 94542
ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interdisciplinary Center for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 21; Length 583;
Pred. No. 2.86e-31;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 others
Plant Mol. Biol. 26, 1085-1101 (1994)
95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-mail: robferl@nervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: cbaysdor@s1.csuhayward.edu
                                                                                                                                                                                                                                                    fax: 602-621-7186
E-mail: helnjars@ccit.arizona.edu
                                                                  Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g2415636
EST; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
                                             Other_ESTs: 05c04d02-f21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing Core
University of Florida
P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.4%;
Best Local Similarity 88.0%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .>583
104 c
                                                                                                                                                                                                                                                                                                                                                                                                                                       fax: 510-727-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rob
```

source

FEATURES

φ

RESULT 11

g õ DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

BASE COUNT ORIGIN

mRNA

ö

Gaps

ö

1 others

į

```
/note="Vector: ZipLox; Site_1: Sall; Site_2: NotI; ds-cDMA
was prepared from oligo-dr selected mRNA by priming with a
NotI oligo-dr oligomer and then adding the second strand
to RNAse-nicked DNA.RNA hybrid with DNA Poll. Sall
adaptors were added to the ends, the ds-cDNAs were then
digested with NotI and size-selected. These were
directionally-cloned into the ZipLox phage vector, excision
as plasmids, and then individually analyzed."
/db.xref="taxon:457"
/clone="5Codes"
/clone="5Codes"
/clone="5Codes"
/lab_host="membrane-free polysomes from endosperm"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mueller-Pillasch, F., Zimmerhackl, F., Geng, M. and Gress, T.M. Direct Submission
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm, Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homos sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
( bases 1 to 360)
Gress, T.M., Muller-Pillasch, F., Geng, M., Zimmerhackl, F., Zehetner, G., Friess, H., Buchler, M., Adler, G. and Lehrach, H. A pancreatic cancer-specific expression profile
Oncogene 13 (8), 1819-1830 (1996)
      of Biological Sciences, School of Science
State University, Hayward
                                                                                                                                                                     Interdisciplinary Center for Biotechnology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .360
/organism="Homo sapiens"
/hote="overexpressed in pancreatic cancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 21; Length 163
Pred. No. 1.59e-29;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ų
                                                                                                                                                                                                                                P.O. Box 100695
Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
E-mail: robferinervm.nerdc.ufl.edu
                                             Hayward, CA 94542
ph: 510-881-3459
[Eax: 510-727-2035
E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human clone xs366 mRNA sequence. U46550 g1236492
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="W64A2"
                                                                                                                                                                                         DNA Sequencing Core
University of Florida
P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.2%;
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1. .>163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 360)
      Department of California Sta
                                                                                                                                                                                                                                                                                                                                                                                  Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                    Ferl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                    Rob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                /organism="Zea mays"
/strain="W64A2"
/note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
/note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT oligomer and then adding the second strand
to RNase-nicked DNA:RNA hybrid with DNA PolI: SalI
adaptors were added to the ends, the ds-cDNAs were then
digested with NotI and size-selected. These were
directionally-cloned into the ZipLox phage vector, excised
as plasmids, and then individually analyzed."
/clone="ScO2HOI"
/clone="ScO2HOI"
/lab_nose="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
fax: 602-621-7186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T18683 163 bp mRNA EST 17-0CT-1996
5CO4ED2-T7 membrane-free polysomes from endosperm Zea mays CDNA
Clone 5CO4ED2 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 CAGGIACCGGICCGGAAITCCCGGGICGACCCACGCGTCCGGAIGCAAGNANGNGNCNAN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae: mitochondrial eukaryotes: Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 21; Length 669
Pred. No. 2.86e-31;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lbraries
lant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 t
Gainesville, FL 32611-0695
ph: 904-3921-1928, ext. 301
fax: 904-392-4072
E-mail: robferlnervm.nerdc.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: The Maize cDNA Project
                                                                                                                          Seq primer: T7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.8%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <1. .>669
118 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chris Baysdorfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Larkins, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9485613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ag 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
```

g ò

용 ö ö

Gaps

ö

```
/organism="Zea mays"
/strain="W64A2"
/note="Vector: ZipLox; Site_1: Sall; Site_2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
Elkaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 364)
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
                                                                                                                                                                                                                                                                                                                                      T14653 364 bp mRNA EST 17-0CT-1996 05c03g08-f21 membrane-free polysomes from endosperm Zea mays cDNA clone 05c03g08 3' end similar to starch branching enzyme II, mRNA
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ,85721
ph: 602-6218-746
fax: 602-621-7186
E-mail: helnjars@ccit.arizona.edu
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larkins, B.
Partial sequencing and mapping of clones from two maize cDNA
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biological Sciences, School of Science California State University, Hayward Hayward, CA 94542
ph: 510-881-3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for Biotechnology Research
                                                                                                                                       Length 360;
                                                                                others
                                                                                                                                                                              2; Indels
                                                                                16
                                                                                                                                                                                                                                       16 caggtancggtcaggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                   27 CAGGIACCGGICCGGAAIICCCGGGICGACCCACGCGICCG 67
/db_xref="taxon:9606"
/cell_line="Patu 8988t"
/tissue_type="pancreatic cancer"
/clone="xs366"
95 c 129 g 67 t 1
                                                                                                                                     Score 38; DB 23; 1
Pred. No. 1.59e-29;
0; Mismatches 2.
                                                                         ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Mol. Biol. 26, 1085-1101 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
E-mail: robferl@nervm.nerdc.ufl.edu
Seq primer: F21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fax: 510-727-2035
E-mail: cbaysdor@sl.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: The Maize cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                           129 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interdisciplinary Center DNA Sequencing Core University of Florida P.O. Box 100695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: 05c03g08-t7
                                                                                                                                     8.2%;
llarity 95.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chris Baysdorfer
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
T14653
9440632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95111093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rob Ferl
                                                                             53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maize.
                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
COMMENT
                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                     RESULT
```

Ì

```
NotI oligo- dr oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Poll. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."

//db.xref-"taxon:4577"
/clone="1050308"
/clone="1050308"
/lab_host="1DH108"
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                          Length 364;
                                                                                                                                                                                                                                                                      Score 38; DB 21; Length 364
Pred. No. 1.59e-29;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                   CGGACGCGTGGGTCGACCCGGGAATTCCGGACCGGTACCTG 293
                                                                                                                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                  93
                                                                                                                                                                                              . .>364)
86 g
                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: Mon Mar 8 22:09:57 1999 Job time : 1537 secs.
                                                                                                                                                                                                complement(<1.
                                                                                                                                                                                                                                                                      Query Match 8.2%;
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                    U
                                                                                                                                                                                                                  94
                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                   253
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                       Сp
```

ò g

(TM)
<u> </u>
<u></u>

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 n.a. database search, using Smith-Waterman algorithm n.a.

Mon Mar 8 22:10:16 1999; MasPar time 74.90 Seconds 851.874 Million cell updates/sec Run on:

not generated. Tabular output

>US-09-206-040-1 (1-469) from US09206040A.seq 465 Description: Perfect Score:

ttaacttgcagcgnccaggt.......gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.......ctactatgtaacttctanna 1 ttaacttgcagcgnccaggt. N.A. Sequence:

Scoring table:

TABLE default Gap 6

188442 segs, 68026449 bases x 2 Query 0 Dbase 0; Nmatch STD Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

Database:

n-geneseg32 l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part24 30:part30 31:part31 32:part32 33:part33 34:part34 40:part40

Mean 8.266; Variance 4.624; scale 1.788 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

						CHUMBLES		
			ф					
Result	۲,		Query					
ž	No.	Score	Match	e Match Length DB]	DB	ΩI	Description	Pred. No.
່ວ	-	39	4.8	204	-	N81164	Base substituted E.co	1.27e-10
	~	38	8.2	91	6	051746	Oligonucleotide probe	5.35e-10
υ	m	38	8.3	91	σ	051746	Oligonucleotide probe	5.35e-10
	4	38	8.2	570	37	T91275	cDNA encoding a novel	5.35e-10
	'n	38	8.2	696	38	T96721	Human synaptogyrin cD	5.35e-10
	ဖ	38	8.5	1581	22	T32233	Cuphea C14:0-ACP thio	5.35e-10
	^	38	8.3	1698	40	V17199	Human MKK3-interactin	5.35e-10
	ထ	34	7.3	204	ч	N81164	Base substituted E.co	1.52e-07
	6	32	6.9	114	12	070468	Generic DNA sequence	2.39e-06
. •	10	30	6.5	114	12	070465	Generic DNA sequence	3.58e-05
	11	30	6.5	114	12	070467	Generic DNA sequence	3.58e-05
υ	12	30	6.5	114	12	070467	Generic DNA sequence	3.58e-05
υ	13	53	6.2	114	12	070468	Generic DNA sequence	1.36e-04

C 14 29 6.2 114 12 070465 Generic DNA sequence 6.0 114 12 070466 Generic DNA sequence 6.0 114 12 070466 Generic DNA sequence 7 18 28 6.0 114 12 070466 Generic DNA sequence 6.0 114 12 070466 Generic DNA sequence 7 19 27 5.8 114 12 070470 Generic DNA sequence 7 19 27 5.8 114 12 070470 Generic DNA sequence 7 10 27 5.8 2606 32 772895 Plasmodium E31a gene. 2 2 2 7 5.8 2606 14 083527 Plasmodium E31a gene. 2 2 2 2 5.6 10 32 775702 Generic DNA sequence 7 2 2 2 5.6 168 32 775470 Generic DNA sequence 7 2 5.6 5.6 114 12 070466 Generic DNA sequence 7 2 5.7 5.8 5.4 114 12 070470 Generic DNA sequence 7 2 5.4 114 12 070471 Generic DNA sequence 7 5.4 114 12 070471 Generic DNA sequence 7 5.4 114 12 070471 Generic DNA sequence 7 5.4 114 12 070472 Generic DNA sequence 7 5.4 114 12 070473 Generic DNA sequence 7 5.4 5.2 114 12 070473 Generic DNA sequence 7 5.4 5.2 114 12 070473 Generic DNA sequence 7 5.2 5.4 14 12 070473 Generic DNA sequence 7 5.2 5.4 5.5 6 035072 Generic DNA sequence 7 5.2 5.4 5.5 6 035072 Human endothelin-lin and 8 5.2 5.4 5.5 6 035072 Human endothelin-lin and 8 5.2 5.4 5.2 114 12 070473 Generic DNA sequence 7 5.2 14 12 070473 Generic DNA sequence 7 5.2 14 12 070473 Generic DNA sequence 1	1.36e-04 5.06e-04 5.06e-04	.06e-	1.86e-03	1.86e-03 1.86e-03	1.86e-03	1.86e-03	ø.		œ.	•	2.350-07	۳.	Ĕ.	2.36e-U2	2.36e-02	8.19e-02	ᅼ	8.19e-02	.19	8.19e-02	۲.	2.78e-01	2.78e-01	•	.78	.18	.18e-	9.18e-01
14 29 6.2 114 12 070 15 28 6.0 114 12 070 18 22 86.0 114 12 070 19 27 5.8 114 12 070 20 27 5.8 2606 32 176 21 27 5.8 2606 31 081 22 22 27 5.8 2606 31 081 23 27 5.8 2606 31 081 24 26 5.6 190 32 176 25 26 5.6 190 32 176 26 26 5.6 114 12 070 27 28 28 200 36 178 28 28 28 200 31 176 29 25 5.4 114 12 070 31 25 5.4 114 12 070 31 25 5.4 114 12 070 32 24 5.2 114 12 070 33 24 5.2 114 12 070 34 24 5.2 114 12 070 35 24 5.2 114 12 070 36 27 64 18 21 171 37 24 5.2 184 12 070 38 23 4.9 82 21 171 41 22 3 4.9 180 32 176 42 22 4.7 75 21 171 44 22 4.7 89 32 176	DNA	DNA sequenc	DNA sequenc	DNA sequenc ium E31a qen	E3la g	vecto	Generic DNA sequence		se antisense ol	oligonucleotid	O	c DNA	DNA	endothelin-1	envelope region	TSAR library	TSAR library	DNA sequen	C DNA	DNA	ast Constituent	TSAR library	3 TSAR library	vascular cel	antisense	TSAR library	3 TSAR library	n ILS antisense
14 29 6.2 114 15 28 6.0 114 18 28 6.0 114 20 27 5.8 114 21 27 5.8 200 22 27 5.8 200 23 27 5.8 200 24 26 5.6 110 25 26 5.6 110 26 26 5.6 110 27 28 5.1 114 30 25 5.4 114 31 25 5.4 114 31 25 5.4 114 32 24 5.2 114 34 24 5.2 114 35 24 5.2 114 36 24 5.2 114 37 24 5.2 114 38 23 4.9 130 41 23 4.9 130 42 22 4.7 75	000	, 0 0	070470	0/04/0 T72895	083527	T75702	046	T76270	T76452	051787	970471	970472	070472	T76405	507	T13613	T13611	047	047	070471	011195	T13612	T13610	T76152	645	36	36	762
14 29 6.2 111 28 6.0 111 18 28 6.0 111 18 28 6.0 111 19 22 22 22 22 27 5.8 200 122 22 22 22 27 5.8 200 123 22 22 22 22 22 22 22 22 22 22 22 22 2	122	322	175	35	14	36	12	32	32	^	12	12	12	32	9	21	21	12	12	12	~	21	21	32	32	21	21	32
115 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	114	114	114	2606	2606	5030	114	168	190	39	114	114	114	178	9	74	81	ч	-1	М	36	75	85	m	σ	75	81	89
114 115 116 117 118 118 118 119 119 119 119 119 119 119					٠	٠	٠		•					•	•	•	•		•				•		•	•	•	
42211111111111111111111111111111111111	DDU		u , :	,, u,	ш,	ш,	ш,	u)	41	ш,	ш,	u ,	u 1	4,	uı	u,	u i	u,	יש	ω,	4	4	4	4	4	4	4	4
	23.0	28 28 28 28	27	. 22	27	27	56	56	56	22	25	25	25	25	52	24	24	24	24	24	23	23	23	23	23	22	55	22
	15	17 18	19	270	22	23	24	52	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
	U	ပပ		υ			O	O	U				O			O	O		υ	O				O		U		

ALIGNMENTS

```
Introducing random point mutations into nucleic acods introducing random point mutations into nucleic acods in introducing random point mutation, completion of molecules and screening.

This is a singlish in the second into the alpha fragment of soliciosure; p; English were introduced into the alpha fragment of E coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The course transcriptase. Nucleotides are usis no specified region. The reverse transcriptase and the molecules are completed to forms that can be transcriptase and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which see also P80575.
                                   N81164;
08-NOV-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                    05-MAY-1988; 105163.
30-MAR-1888; 105163.
03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P. Knowles J. Koivula A. Bamford J. Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                               /*tag= a
/function=multiple cloning site
187.204
/*tag= b
                                                                                                                            Location/Qualifiers
                    BP
RESULT 1
ID N81164 standard; DNA; 204
                                                                                                                                                . 69
                                                                                                                                          misc_feature
                                                                                                                                                                                                primer_bind
                                                                                                                                                                                                                                     EP-285123-A
```

108 Others;

11 T;

ö 11

47 C;

21 A;

204 BP;

Sequence

N

```
91 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                            W09739126-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1998
 Sequence
                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                          셤
                                                                           Sp
                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                              87 mrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvh 146
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MK14
but
                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                               Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q5175). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 14: 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                      nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                               31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligo:nucleotide probes specific for Mycobacteria – used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                     New oligo:nucleotide probes specific for Mycobacteria – use detection and amplification of Mycobacteria nucleic acid in
        Score 39; DB 1; Length 204; Pred. No. 1.27e-10;
                            52; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Length 91;
                                                                                    147 nhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvhccv 188
                                                                                                                                                                                                                                                                                                                                                                           4 ∃;
                                                                                               Score 38; DB 9; L
Pred. No. 5.35e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           15 G;
                                                                                                                                                                                                                                                                                                                                                                          17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .T 3
Q51746 standard; cDNA; 91 BP.
                                                                                                                                               BP.
                                                                                                                                                                                                                         01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                            8.28;
                                                                                                                                                                                                                                                                                                                                                                                                      larity 4.0%;
Conservative
         Query Match 8.4%;
Best Local Similarity 13.7%;
                            Conservative
                                                                                                                                              standard; cDNA; 91
                                                                                                                                                                                                                                                                 Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          91 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
EP-571911-A.
01-DEC-1993.
                              14:
                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                        samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    051746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sambles
                                                                                                                                             051746
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                            Matches
                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                   Сp
                                                                                    셤
                                                                                                       Cp
                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

```
designated PIEC. The protein has Cys residues of a beta-chemokine (C32, designated PIEC. The protein has Cys residues of a beta-chemokine (C32, C33, C56 and C72). The present sequence was isolated from a CDNA library generated from non-tumourous human prostate tissue. The PTEC protein is a homologue of human RANTES, which is a C-C chemokine with structural similarity to interleukin-8 and human MIP-libeta. The polynucleotide sequence encoding PIEC can be used to diagnose or treat a condition associated with the presence of activated T cells including viral, bacterial, fungal or helminthic infections, allergic or asthmatic responses, mechanical injury associated with trauma, arteriosclerosis, atherogenesis or collagen vascular diseases, autoimmune diseases such as themmatoid arthritis, myasthenia gravis, systemic lupus erythematosus or haemolytic anaemia, leukaemia, laymphomas or carcinomas, and diseases of immediate type hypersensitivity which involve activation or excessive cosinophils, basophil, mast and T cells.

Sequence 570 BP; 149 A; 155 C; 138 G; 128 T;
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                           Gaps
                                                                                                                                                           2 gctccggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvc 61
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synaptogyrin; human; colon cancer; lung cancer; brain tumour; Crohn's disease; rheumatoid arthritis; AIDS; allergy; urticaria; juvenile diabetes; scleroderma; antisense; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTEC, a novel human beta-chemokine - useful for diagnosing and treating e.g. viral, bacterial, fungal infections, auto-immune diseases, etc
                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           chemokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immediate type hypersensitivity; leukocyte proliferation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                           11; Indels
                                                     Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding a novel beta-chemokine designated PTEC Beta-chemokine; PTEC; homologue; human RANTES; C-C cl diagnosis; treatment; activated T cell;
  4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caggtaccggtactggaattcccgggtcgacccacgcgtccg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 37; ]
Pred. No. 5.35e-10;
0; Mismatches 2.
                                                                               Pred. No. 5.35e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                           42; Mismatches
  15 G;
                                                     Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Pages 39-40; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
110..784
17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE PHARM INC.
Bandman O, Hawkins PR, Murry LE;
WPI; 97-526462/48.
P-PSDB; W27271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .r 5
T96721 standard; cDNA; 969 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                        J. 4
T91275 standard; cDNA; 570
T91275;
                                                     8.2%;
11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                            Query Match
Best Local Similarity 11.7%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                23-APR-1998 (first entry)
5 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human synaptogyrin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1997; U06249.
17-APR-1996; US-633682.
```

```
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA.
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        WO9800539-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIP-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                           V17199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
ID NB
AC NB
DT 08
DE BB
KW E.
OS EE
                                                                         g
                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant produ. of myristate in plant cells - using DNA with preferential activity on C14 fatty acids from Cuphea palustris, and med camphor, useful in detergent and food industries in turneg and camphor, useful in detergent and food industries. Example 1: Fig 1A-1E: 77pp; English.

A CDNA clone (732233), designated MCT34 (pCpFatB2), codes for Cuphea palustris C14:0-ACP thioesterase (W2081), an enzyme that acts primarily on C14:0-ACP substrates. forming C14:0 (myristate). It was isolated from a developing seed CDNA library by screening with sequences encoding medium-chain acyl-ACP thioesterases from Cuphea cookeriana. Constructs for expression of clone MCT34 in plant seeds under the control of napin or oleosin regulatory regions were prepd. These allow high-level produ. of myristate (useful in surfactants and foods) in plant cells, e.g. Brassica.
                                                                                                                                                                                This polynucleotide (snpg) identifies and encodes a novel human synaptogyrin homologue (SNPG) (see W36516). It was initially cidentified in Incyte Clone 775426 from a colon cDNA library (count) prepared from a Crohn's disease patient. Also claimed are: (1) an expression vector containing PN: (2) a host cell are: (1) an expression vector of (1): (3) the purified 224 amino acid SNPG protein: (4) an antisense molecule complementary to PN: (5) an antisense molecule complementary to PN: (5) an antibody (Ab) specific for the polypeptide of (3): Human SNPG can be used for the diagnosis and treatment of a disease associated with synaptogyrin, especially Crohn's disease, rheumatoid arthritis, asthma and cancers or tumours of the lung, colon or brain (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                               P-PSDB; W36516.
Novel human synaptogyrin homologue - useful for diagnosis and
treatment of, e.g. rheumatoid arthritis, Crohn's disease, cancers,
                                                                                                                                                                                                                                                                                                                                                                              AIDS, allergy, urticaria, juvenile diabetes, scleroderma, etc. Sequence 969 BP; 163 A; 324 C; 280 G; 202 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-071-1996 (first entry)
Cuphea C14:0-ACP thioesterase CDNA clone MCT34 (CpFatB2).
Myristate: myristic acid; fatty acid; acyl-ACP thioesterase; seed oil; oilseed; vegetable oil; Brassica; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ë
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.2%; Score 38; DB 38; Length 969
Best Local Similarity 95.1%; Pred. No. 5.35e-10;
Dest Local Similarity 95.1%; Pred. No. 5.35e-10;
On Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 caggtaccggtccggaattcccgggtcgacccacgcgtccg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 caggtancggtcaggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in plant cells, e.g. Brassica.
1581 BP; 418 A; 356 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                          Claim 2; Page 46-47; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1995; US-383756.
05-JUN-1995; US-460898.
(CLJ) CALGENE INC.
Dehesh K, Hawins D, Voelker TA;
WPI; 96-371439/37.
                                                     30-APR-1996; US-700637.
(INCY-) INCYTE PHARM INC.
Hawkins PR, Murry LE, Stuart SG;
WPI; 97-549677/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .T 6
T32233 standard; cDNA; 1581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119..1354
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-1996.
01-FEB-1996; U01585.
                           06-NOV-1997.
30-APR-1997; U07378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuphea palustris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surfactant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W02081
               WO9741143-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9623892-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
PF P-ESDB; W52169.

R P-ESDB; W52169.

Human MKK3-interacting protein, used to identify human tissues in malignant conditions - comprises nucleic acid, antibodies, fusion malignant conditions - comprises nucleic acid, antibodies, fusion proteins and peptide fragments

Proteins and peptide fragments

Proteins and peptide fragments

Disclosure; Page 14; 17pp; English.

C This CDNA encodes a human MKK3-interacting protein (MIP). The mitogen-activated protein kinase (MARX) interacting an protein kinase that cativated protein kinase specifically and is involved in transducing stress signals. The MIRX and may be involved in transducing interfering mutant form of MKK3 and may be involved in transducing extracellular signals to the nucleus, resulting in activation of p38 (finase: MIP is expressed in human brain, kidney, liver, lung, pencreas and spleen but not in heart or striated muscle: Detection of MIP in a body sample (particularly a tumour or metastasis) is used to identify the tissue selected from the group consisting of brain, kidney, liver, lung, pencreas or spleen tissue. Fusion proteins comprising at least 8 contiguous amino acids of MIP fused to a second protein sequence can be used to target MIP, or its peptides, to specific cells or tissues. They can be used as a source of MIP in assays and also as munuogen. The MIP encoding nucleic acid is used for expression of munuogen. The MIP polypeptides and as a source of probes for detecting
                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                      V17199;
10-JUN-1998 (first entry)
Human MKK3-interacting protein (MIP) encoding cDNA.
MKK3-interacting protein; MIP; mitogen activated protein kinase;
MKR3-interacting protein; MIP; mitogen activated protein kinase;
MAPK kinase-3; human; transduction; target; extracellular signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NoV-1990 (first entry) assessible alpha-fragment. Base substituted E.coli beta-galactosidase alpha-fragment; base substitutions; ss. Escherichia coli
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 T;
                Length 1581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1698;
Score 38; DB 22; Lens. Pred. No. 5.35e-10; Pred. No. 5.35e-10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167..1213
/*tag= a
/product= "MKK3-interacting protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 caggtaccggtccggaattcccgggtcgacccacgcgtccg 102
                                                                                                                                                                           449 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.35e-10;
0; Mismatches 2
                                                                                                                                          41 caggtaccggtccggaattcccgggtcgacccacgcgtccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Score 38; DB 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            standard; cDNA; 1698 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N81164 standard; DNA; 204 BP. N81164;
                Query Match
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 95.1%;
hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1998.
02-JUL-1997; U10866.
01-JUL-1997; US-886572.
03-JUL-1996; US-02124.
12-JUL-1996; US-021641.
(CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kavanaugh MW, Shyamala V;
WPI; 98-086965/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interfering mutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1698 BP;
```

```
(SUSSO) SUOMEN SOKERI OY.

Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;

WPI; 88-27992740.

Introducing random point mutations into nucleic acods -

Throducing random point mutations into nucleic acods -

Dy prepn of single stranded template, annealing a primer, elongation,

The misincorporation, completion of molecules and screening.

Disclosure; p: English.

Englis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure: Page 35; 255pp; English: Comprise Compr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 rbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbn 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 070468;
05-APR-1995 (first entry)
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcagcgnccaggtancggtcaggaattcccgggtcgacccacgcgtccgtacggctgcga 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/*tag= a
//note= "this sequence represents '2'; Z can be a
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 204; Pred. No. 1.52e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 T;
                                                /function-multiple cloning site 187..204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 nhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aagacgacagaaggggggggaaagaga 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UXNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q70468 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.38;
5.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                     *tag= a
                                                                                                                                                  /*tag=
                                                                                                                                                                                                                  05-MAY-1988.
30-MAR-1988; 105163.
03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55..60
/*tag=
   19..69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fowlkes DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9418318-A.
                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
```

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins screening a binding domain and an effector domain bischosure; Page 35, 255pp; English.

Q70465 is a generic DNA sequence used to generate random TSAR (Totully Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)6TGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that ore specific peptides generated by these generic sequences are shown in Q70466-6R. Other specific peptides generated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with ö 308 tecegegetecteateteceatgttegeceaetttegettetatetaegtegetggaagget 367 0.5-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss. 3 banbanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbanan Gaps Ø /*tag= a
/note="this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)" 368 gtggcaggacgcagagaatcgcgtttatctcatcaaagagctcgataggatc 419 63 bnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114 Length 114; 76; Indels Score 32; DB 12; I Pred. No. 2.39e-06; 32; Mismatches 76; Location/Qualifiers JT 10 Q70465 standard; DNA; 114 BP. 11-FEB-1993; US-013416. 30-DEC-1993; US-176500. 31-JAN-1994; US-189331. (UXNC-) UNIV NORTH CAROLINA. FOWNKES DM, KAY BK; 6.9%; 3.6%; 4; Conservative WPI; 94-279739/34. P-PSDB; R65150 and R65151. 55..60 Best Local Similarity misc_feature 01-FEB-1994; WO9418318-A Synthetic. Query Match 070465; Matches 888888888888888888888888888 셤 ŏ g ò

```
Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35: 255pp; English.

COM667 is a generic DNA Sequence used to generate random TSAR (Totally

COM667 is a generic DNA Sequence used to generate random TSAR (Totally

COM667 is a generic DNA Sequence used to generic formula can also be

COM667 is a generic DNA Sequence used to generic formula can also be

COM76667 is a generic DNA Sequence used to generic formula can also be

COMPRISIONEDIA (TOTAL) IN A TABLE OF TOTAL OF T
chemically or aligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonoucleotides are also designed so that the expressed peptide contains. The oligonoucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or blodogically active molety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody activity allowing direct and rapid detection in a screening process. Sequence 114 BP: 0 A; 2 C; 2 C; 2 I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 gggcaataatcgatcccgcattcccgcgctcctcatctccatgttcgccactttcgcttc 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 banbanbanbanbanbanbtqcaabanbanbanbanbanbanbanbanbanbanban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "this sequence represents '2'; 2 can be a sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 tatctacgtcgctggaaggctgtggcaggacgcagagaatcgcgtttatctc 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 12; Pred. No. 3.58e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence of 6, comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q70467 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U00977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 94-279739/34.
P-PSDB; R65153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1994.
01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9418318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   070467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
```

```
Terentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

Comprising a generic DNA sequence used to generate random TSAR (Totally Disclosure, Page 35; 255pp; English.

Comprising a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: x(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)17; x and Y are flanking restriction Sites (X is not the same as Y) that are controlled further. Other generic sequences are shown in CR5151-54. TSARS are concatenated by these generic sequences are shown in CR5151-54. TSARS are concatenated by these generic sequences are shown in CR5151-54. TSARS are concatenated by these generic sequences are shown in CR5151-54. TSARS are concatenated by these generic sequences are shown in CR5151-54. TSARS are concatenated by these generic sequences are shown in CR5151-54. TSARS are concatenated by these generic sequences are shown in CR5151-54. TSARS are concatenated by they may further comprise a linker peptide between the 2 domains. They may further comprise a linker peptide between the 2 domains. They may further comprise a linker to the upredicted or variant residues. These residues conformational arguminator sequences. They can be comprised by a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion.

CR11. They can also replace the function of macromolecules, eg.

CR11. They can also replace the function of macromolecules, eg.

CR11. They can also replace the function of macromolecules, eg.

CR11. They can also replace the function of macromolecules, eg.

CR11. They can also replace the function of macromolecules, eg.
deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                    305 cattocogogotoctcatctccatgttcgccactttcgcttctatctacgtcgctggaag 364
                                                                                                                                                                                                                                                                                                                      Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain: effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can
                                                                                                                                                                                                                           Length 114;
                                                                                                                                                                                                                      Score 30; DB 12; Length 114
Pred. No. 3.58e-05;
31; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "this sequence represents '2'; Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 gctgtggcaggacgcagagatcgcgtttatctcatcaaagagctc 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                 direct and rapid detection in a screening process Sequence 114 BP; 0 A; 2 C; 2 G; 2 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                                                                                                                                                      Query Match
Best Local Similarity 1.9%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          r 12
Q70467 standard; DNA; 114
Q70467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-013416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1994.
01-FEB-1994; U00977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 94-279739/34.
P-PSDB; R65153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9418318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
     888888888
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
```

```
PF PERSB: R65154.

PT Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptide(s) which bind a ligand - by
Identifying proteins or peptides. Library expressing fusion proteins
PT Screening a recombinant vector library expressing fusion proteins
PD Solosure, Page 35; 255pp; English.

Disclosure, Page 35; 255pp; English.

CC ONTOKES is a generic DNA sequence used to generic formula can also be
CC represented as follows: X(NNB)1(TGC)(NNB)52(NNB)7(TGC)(NNB)10Y. X

and Y are flanking restriction sites (X is not the same as Y) that are
CC order specific peptides generated beterofunctional proteins or peptides.

CC other specific peptides generated heterofunctional proteins or peptides.

CC offer specific peptides generated heterofunctional proteins or peptides.

CC offer specific peptides generated heterofunctional proteins or peptides.

CC offer sing at lagand and a second effector peptide portion that is
CHEMICALLY TARRS are concatenated heterofunctional proteins or peptides.

CC offer some degree of Gonains. The Oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
in, or flanking, the unpredicted or variant residues. These residues
CC offer some degree of Conformational rigidity to the peptides. The TSARs

CC confer some degree of Conformational rigidity to the peptides.

CC deliver a chemically or biologically active moiety, eg. metal ion,

CC addiver a chemically or biologically active moiety, eg. metal ion,

CC addiver a chemically or biologically active moiety, eg. metal ion,

CC addiver a chemically or biologically active moiety, eg. metal ion,

CC comprise methods of hybridoma formation or in vivo antibody

CC complex methods of hybridoma formation or in vivo antibody

CR complex methods of hybridoma formation or in vivo antibody

CR allowing direct and rapid detection in a screening process.

CR 2 C; 2 C; 2 C;
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                  Q.P.PR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                       ctttggtgctgctgctacttttctggtcaagaaagtcaccaagaatccactcttt 89
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
//note= "this sequence represents '2'; 2 can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                ö
                                                                                30; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
                                         Length 114;
                                                                                                                                                                                                          69 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtg 110
                                                                                                                                                                                                                                  ccccccctttgtcgtctttcgcagccgtacggacgcgtg 47
                                                          Pred. No. 3.58e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 12;
Pred. No. 1.36e-04
                                         DB 12;
2
G;
                                         Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
2
C;
                                                                                                                                                                                                                                                                                                                                    Q70468 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, RAY BK;
WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%;
1.8%;
                                       6.5%;
0 A;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-013416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2; Conser
                                       Query Match
Best Local Similarity
114 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994;
01-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9418318-A
  Sequence
                                                                                                                                                                                                                                                                                                                                                            070468;
                                                                                                                                                              148
                                                                                                                                                                                                                                                   88
                                                                                  Matches
                                                                                                                                                                                                                                                                                                              S
                                                                                                                         g
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                   ζb
                                                                                                                                                              ç
```

```
rereals, noison and woison.

Freeling a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

Comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

COMA65 is a generic DNA Sequence used to generate random TSAR (Totally

COMA65 is a generic DNA Sequence used to generate random TSAR (Totally

COMA65 is a generic DNA Sequence used to generic formula can also be

represented as follows: X(NNB)6(TGC)(NNB)11Z(NNB)4(TGC)(NNB)3Y. X

COMAFISTOR TEAR TO THE GENERIC SEQUENCES ARE SHOWN in Q70466-68.

COTHER Specified further. Other generic sequences are shown in Q70466-68.

COTHER Specified further of a generic sequences are shown in CR6151-54. TSARS are concatenated beterofunctional proteins or peptides,

COTHER SPECIFIED SECTION STATES AND SECTION STATES AND SECTION SECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                  Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
149 tetttggtgetgeggttgetaettttetggtcaagaaagtcaccaagaatccaetett 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can
                                                                    66 banbanbanbanbtgcanbanbanbanbanbanbanbanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                             88 cccccccttctgtcgtcgtcgccgtacggacgcgtggtcgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 banbanbanbanbanbanbanbanbanbanbtgcanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 tecececettetgtegtetttegeageegtaeggaegegtg 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 12; Le
Pred. No. 1.36e-04;
28; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
55..60
/*tag= a
                                                                                                                                                                                                            Q70465 standard; DNA; 114 BP
Q70465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 4.9%;
Matches 5; Conservative
                                                                                                                                                                                                                                                              05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R65150 and R65151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-013416.
US-176500.
US-189331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1993;
31-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9418318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fowlkes DM,
                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                          RESULT
                                                                                                                                                                                                              ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                    გ
                                                               g
                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

```
Tidentifying a proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT Gemprising a binding domain and an effector domain

Disclosure: Page 35: 255pp: English.

COMPAGE 1s a generic DNA Sequence used to generate random TSAR peptide

COMPAGE 1s a generic DNA Sequence used to generate random TSAR peptide

COMPAGE 1s a generic DNA Sequence used to generate random TSAR peptide

COMPAGE 1s not the same as Y) that are not specified further. This

COMPAGE 1s not the same as Y) that are not specified further. This

COMPAGE 1s not the same as Y) that are not specified further. This

COMPAGE 2s of the same as Y) that are not specified further. This

COMPAGE 2s of the same as Y) that are not specific peptides

COMPAGE 2s of the same as Y) that are not specified further. Other

COMPAGE 2s of the same as Y) that are not specified further. Other

COMPAGE 2s of the same as Y) that is chemically or biologically

COMPAGE 2s of COMPAGE 2s of STAR 2s or COMPAGE 2s or English COMPAGE 2s or English COMPAGE 2s or English COMPAGE 2s or English COMPAGE 2s or COMPAGE 3s or English COMPAGE 3s or En
                                                                                               Generic DNA sequence to generate a random TSAR peptide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct: rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                                                                                                                                                                                                  /*tag= a
/note= "this sequence represents '2'; Z can be
sequence of 6,9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 G;
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection in a screening process.
Sequence 114 BP; 0 A; 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
7 15
Q70469 standard; DNA; 114 BP
                                                  Q70469;
07-APR-1995 (first entry)
                                                                                                                                                                                                                                                          55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                       U00977
                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994;
01-FEB-1993;
RESULT
```

Gaps ö Query Match
6.0%; Score 28; DB 12; Length 114;
Best Local Similarity 2.8%; Pred. No. 5.06e-04;
Matches 3; Conservative 30; Mismatches 73; Indels

ö

269 tcacagactctccagtatgggcaataatcgatcccgcattcccgcgctcctcatctccat 328

6 bnobanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbannannanban

66 btgcanbnabanbnabanbanbanbnabanbnabanbnabanb 111

g

ò

셤 ð 329 gttcgccactttcgcttctatctacgtcgctggaaggctgtgggcag 374

Search completed: Mon Mar 8 22:14:25 1999 Job time : 249 secs.

THIS PAGE BLANK (USPTO)

		(TM)
	·	
	' 	<u>-</u>
		T'//
		 }

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm

Mon Mar 8 22:40:59 1999; MasPar time 739.30 Seconds 1499.157 Million cell updates/sec MPsrch_nn Run on:

>US-09-206-040-1 (1-469) from US09206040A.seq 465 Tabular output not generated. Title:

Description:
Perfect Score:
N.A. Sequence:
Comp:

1 ttaacttgcagcgnccaggt.........gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.........tactatgtaacttctanna

TABLE jmetric Gap 60 Scoring table:

Dbase 0; Query 0 Nmatch STD 602357 seqs, 1181590623 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

16:9b_bal 17:9b_ba2 18:9b_htg 19:9b_in 20:9b_om 21:9b_ov 22:9b_pat 23:9b_ph 24:9b_pll 25:9b_pl2 26:9b_prl 27:9b_pr2 28:9b_pr3 29:9b_ro 30:9b_st 31:9b_sts 32:9b_sy 33:9b_un 34:9b_vi 1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_un 15:em_vi
genbankli0 Database:

Mean 8.428; Variance 2.694; scale 3.128 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	6.08e-11	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09	5.65e-09
	Description	Homo sapiens mRNA for	H.sapiens STS, 367bp,	H. Sapiens (xs16) mRNA,	Human tazarotene-induc	Arabidopsis thallana m	Mus musculus Nm1 mRNA,	Arabidopsis thaliana r	Arabidopsis thaliana m	Arabidopsis thaliana p	Sequence 1 from patent	Petunia hybrida mRNA f	Mus musculus pregnane	Mus musculus COP9 comp
	ΩI	AB016247	HSRSTS367	HSXS16	HSU77594	AB010946	AF019249	AF034255	ATRSP40	AF062916	160018	AB000453	AF031814	AF071316
	DB	28	31	27	27	24	53	25	24	25	22	24	53	53
	Ouery Match Length DB	2125	367	372	770	1009	1214	1372	1382	1493	1581	1640	1709	1779
æ	Ouery Match	6.5	9.0	9.0	9.0	0.9	0.9	0.9	0.9	9.0	0.9	9.0	9.0	6.0
	Score	30	28	28	28	28	28	28	28	28	28	28	28	28
	Result No.	-	~	m	4	Ŋ	φ	7	ω	σ	10	11	12	13

5.65e 5.65e 6.
Vigna unguiculata phos Cuphea pulcherrima 3-k Homo saptens monocyte/Human pephBGT-1 betain Human telomerase assoc Arabidopsis thaliana m. X.laevis mRNA for co Coryctolagus cuniculus Arabidopsis thaliana a Sequence 11 from paten Danio rerio mRNA for specine growth hormone Arabidosis thaliana a Sequence 11 from paten Danio rerio mRNA for specine growth hormone Arabidosis thaliana a Sequence 3 from patent Mus musculus FK506 bin Mus musculus Chicken colviA2 gene fhomo sapiens chromosom Arabidopsis thaliana D H. sapiens mRNA for CCA Xenopus laevis growth R. norvegicus mRNA for pGEX-472 cloning vecto pGEX-5X3 cloning vecto pGEX-5X3 cloning vecto general man BAC clone RG119H
AF071862 AF060518 AF060518 AF060518 HSUZA699 ATNABIND XIAMAATP ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39783 ATU39785 AF090334 AF090334 AF022992 GGCCLVIA AF022364 AF022364 AF023364 AF03364 AF03745 AF06462 AF06462 AF0774 AF06462 AF0774 AF06462 AF0774
20000000000000000000000000000000000000
2111 2875 2875 2875 3410 1500 1669 2244 1627 1627 1627 1627 1627 1627 1627 1627
$\begin{array}{c} 000000000000000000000000000000000000$
mmmmmmm4444444444444444444444444444444
1115 1116 1116 1116 1116 1116 1116 1116
000

ALIGNMENTS

AB016247 2125 bp mRNA PRI 09-0CT-1998 Homo sapiens mRNA for sterol-C5-desaturase, complete cds. 48016247 93721881. sterol-C5-desaturase; C5D. Homo sapiens (strain:caucasian) 9-year old female liver cDNA to	Monto sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (sites) Matsushima,M., Inazawa,J., Takahashi,E., Suzumori,K. and	Molecular cloning and mapping of a human cDNA (SC5DL) encoding a protein homologous to fungal sterol-C5-desaturase Cytogenet. Cell Genet. 74 (4), 252-254 (1996) 97130614 2 (sites) Nishino, H. and Ishibashi, T. Nishino, H. and Ishibashi, T. Wolecular cloning and expression of the human and mouse lathosterol	5-desturase Unpublished (1998) 3 (bases 1 to 2125) Nishino,H. Direct Submission Submitted (09-JUL-1998) to the DDBJ/EMBL/GenBank databases. Hide::: Nishino, Hokkaido University School of Medicine, Department of	Biochemistry: N1S97 Kita-ku, Sapporo, Hokkaido 060-8638, Japan (E-mail:hideakin@med.hokudai.ac.jp, Tel:+81-11-706-5047, Fax:+81-11-706-5169) Location/Qualifiers 12125 /organism="Homo sapiens" /strain="caucasian" /db_xref="taxon:9606" /dev_stage="9-year old"
RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS	TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	FEATURES

 \sim

US-09-206-040-1.rge

gene

conflict

BASE COUNT ORIGIN

```
1 (bases 1 to 372)
Mueller-Pillasch, F., Gress, T., Lehrach, H. and Adler, G.
Differential gene expression in pancreatic cancer. Use of an
automated approach for the large scale isolation and
characterisation of CDNA clones containing differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-Aug-1994) Gress T., University of Ulm, Department of Internal Medicine I, Robert Koch Str.8, 89081 Ulm, Germany, 89081 3 (bases I to 372)
Zerss, T.M., Muller-Pillasch, F., Geng, M., Zimmerhackl, F., Zehetner, G., Friess, H., Buchler, M., Adler, G. and Lehrach, H. Apancreatic cancer-specific expression profile 0ncogene 13 (8), 1819-1830 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/dbone="xait"
/clone="xait"
/dev_ztage="adult"
/dev_ztage="adult"
/tisue_type="pancreas"
/cell_type="ductal adenocarcinoma"
/cell_line="panty 9988s"
/cell_line="xs cDNA lib, pancreatic cancer cell line PATU
   --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141. .372
/note="88% homology to bovine NADH-ubiquinone
oxidoreduktase, GenEMBL-locus gb_om:btubre49 residues
                                                                                                                                                 10-APR-1997
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSU77594 770 bp mRNA PRI
Human tazarotene-induced gene 2 (TIG2) mRNA,
91848263
                                                                                                                                                   PRI
 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 27; 1
Pred. No. 5.65e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 t
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 ggaattcccgggtcgacccacgcgtccg 56
                                                        29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GGAATTCCCGGGTCGACCCACGCGTCCG 30
                                    42 GGAATTCCCGGGTCGACCCACGCGTCCG 69
                                                                                                                                             HSXS16 372 bp RNA
H.sapiens (xs16) mRNA, 372bp.
236812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 1. 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 c
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78-307
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                        9533926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gress, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                             human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
28;
                                                                                                                                                                                                                                                                                                                        Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                ო
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
 Matches
                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                    유
                                                                       ŏ
                                                                                                                                           /product="sterol-C5-desaturase"
/db_xref="PID: d1034688"
/db_xref="PID: g3721882"
/translation="MID/ULRYADYFFTPYYVPATWPEDDIFRQAISLLIVTNVGAYI
LYFFCATLSYYFVFDHALMKHPOFLKNOVRREIKFTVQALPWISLITVALFLLEIRGY
                                                                                                                                                                                                                                         SKLHDDLGEFPYGLFELVVSIISFLFFTDMFIYWIHRGLHHRLVYKRLHKPHIUMKIP
PPRSAHAFHPTDGFLQSLPYHIYPFIFPLHKVVYLSLYILVNIWTISTHOGDFRYPQI
LQPFINGSAHHTDHHFFDYNYGQYFTLWDRIGGSFKNPSSFEGKGPLSYVKEWTEGK
RSSPSGNGCKNEKLFNGEFTKTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-SEP-1996) A.B. McKie, ICRF Molecular Pathology Group,
8th Floor, MRC Cyclotron Bldg, Hammersmith Hosp, Ducane Road,
London, W12 ONN, UK
                                                                                                                                                                                                                                                                                                                                                        et al. Cytogenet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alu-polymerase chain reaction genomic fingerprinting technique identifies multiple genetic loci associated with pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 367) McKle.A.B., Iwamura,T., Leung,H.Y., Hollingsworth,M.A. and Lemoine,N.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 28; Leuy...
6.08e-11;
...a 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 367;
                                                                                                                                                                                                                                                                                                                                /gene="c5D"
/note="deleted in D8518 (Matsushima, M. Coll Genet. 74(4), 252-254 (1996))"
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Chromosomes Cancer 18 (1), 30-41 (1997)
97147122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSRSTS367 367 bp RNA STS
H.sapiens STS, 367bp, sequence tagged site.
Y07966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 31; I
5.65e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .367
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="brain"
/lab_host="E.coli"
/chromosome="17"
               /tissue_type="liver"
32. .981
                                                                                                            /EC_number="1.3.3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g1552329
STS; sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                              /codon_start=
sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="p13.3"
                                                                                       /gene="C5D"
                                                    /gene="C5D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.5%;
Best Local Similarity 100.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 367)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .>367
1. .>367
                                                                       .981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McKie, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                                                                                                                                                                                                              670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
```

N

RESULT

q ò DEFINITION

ACCESSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

AUTHORS TITLE JOURNAL

FEATURES

JOURNAL MEDLINE REFERENCE STS BASE COUNT

US-09-206-040-1.rge

TITLE JOURNAL

FEATURES

gene

AUTHORS

JOURNAL REFERENCE

TITLE

AUTHORS

REFERENCE

```
/codon_start=1
/product="AtRerlB"
/product="AtRerlB"
/db_xref="PlD:d1025726"
/db_xref="PlD:d1025727"
/translation="MEGSGDSGSMATPVQKKVHEAWRVYQYYLDKTTPHSTNRWIGT
LVVFLIYCLRYYSIHGFYIISYGLGTYLLNLIGFLSPLVDPELEVSDCATLPPRGSD
EFKPFIRRLPEFKFWYSMFRFCIAFLMTFFSVFDVPWPILLCYWVUFVLTWRRQ
IAHMIKHKYTPFSIIGKQKYSGRKSSANSGGGSRAD"
12 g 318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="PID:g2425060"
/translation="MDADKDNIKQACDERSAEMDDMRCEQSMGLVHEIMSENKELDEE
IKKLEAELQSDAREFQIKENVPEKKLKLTSVESPKDGCHFSNSSCSFQVSSQILYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVTGIPDELSEEQTRDKLELSFCKSRNGGGEVESVDYDRKSRSAVITFVETGVVDKIL
KKKTYPLYNNOKCHSVAVSPCIERCLEKYQVPSAVSKTVLLTGLEGIPVDEETGEDL
LAIHFORKNNGGGEVEVVKCSLDQSFAAYFKEEAREII"
244 c 314 g 261 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGQALITFEKEEVAQNVISMGNHVVQMEGTPVKVSAHPVPLNTGVRFQVHVDISKMKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1214) . Mehtani, S. and Zervos, A.S. Mouse homologue of the human Nmi cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1214)
Mehtani,S. and Zervos,A.S.
Direct Submission
Submitted (13-AGG-1997) Cutaneous Biology Research Center,
Massachusetts General Hospital, Harvard Medical School, 13th
Street, Bldg. 149, Charlestown, MA 02129, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to H. sapiens Hou encoded by GenBank
Accession Number U32849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guery Match 6.0%; Score 28; DB 24; Length 100
Best Local Similarity 100.0%; Pred. No. 5.65e-09; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DB 29; Length 121
Pred. No. 5.65e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R00
                                               /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1214 bp mRNA
Nmi mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                     /clone_lib="Lambda-PRL2"
152. .739
                                                                /variety="columbia"
/db_xref="taxon:3702"
/clone="143C4T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAATTCCCGGGTCGACCCACGCGTCCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ggaattcccgggtcgacccacgcgtccg
                                                                                                                                                                                                       152. .739
/gene="AtRER1B"
                                                                                                                                                                                  /gene="AtRER1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"Nm1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0%;
Matches 28; Conservative
                     .1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
AF019249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF019249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q2425059
                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                          CDS
    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="tazarotene-induced gene 2"
/db_xref="PID: 01848264"
/tb_xref="PID: 01848264"
/translation="mreliplaturidayGyGyGyAELTEAQRRGLQYALEEFHKHPPVQ
/translation="mreliplaturidayGyGyGyAELTEAQRRGLACI
KLGSEDKYLGRLYHCPIETQYLREAEEHQETQCLRYQRAGEDPHSFYFPGQFAFSKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes galore: a summarror of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol: 106 (4), 1241-1255 (1994)
                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="retinoid (tazarotene) treated and untreated skin graft cultures of foreskin keratinocytes and dermal fibroblasts"
1 (bases 1 to 770)
Nagpat,S., Patel,S., Jacobs,H., DiSepio,D., Ghosn,C., Malhotra,M.,
Nagpat,S., Puvic,M. and Chandraratna,R.A.S.
Teng,M., Duvic,M. and Chandraratna R.A.S.
Tazarotene-induced gene 2 (TIG2), a novel retinoid responsive gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-FEB-1998) to the DDBJ/EMBL/GenBank databases. Ken Sato, The Institute of Physical and Chemical Research(RIKEN), Molecular Membrane Biology Laboratory; 2-1 Hirosawa, Wako, Saitama 351-0106, Japan (E-mail:satoken@postman.riken.go.jp, Tel:+81-48-467-9548, Fax:+81-48-462-4679)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman,T., de Bruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel ,E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                  2 (bases 1 to 770)
Nagpal,S., Patel,S. and Chandraratna,R.A.S.
Direct Submission
Submitted (06-NOV-1996) Biochemistry, Allergan Inc., 2525 Dupont Dr., Irvine, CA 92713, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (variety:columbia) cDNA to mRNA, clone_lib:Lambda-PRL2 clone:143C4T7.
Arabidopsis thaliana
Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; seed plants; Magnoliophyta;
eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (sites)
Satc.K., Ueda.T. and Nakano,A.
Identification of Arabidopsis thaliana RER1 homologues
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 27; Length 770;
Pred. No. 5.65e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA for AtRerlB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GGAATTCCCGGGTCGACCCACGCGTCCG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB010946 1009 bp
Arabidopsis thallana mi
AB010946
92865176
AtRerlB.
                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="TIG2"
97. 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                        97. .588
/gene="TIG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 1009)
Sato, K. and Nakano, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (sites)
                                                                                        in skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95148729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                                                                                                                               source
```

DEFINITION

RESULT

셤 ö ACCESSION

KEYWORDS SOURCE

BASE COUNT

ORIGIN

ORGANISM

REFERENCE AUTHORS

AUTHORS TITLE

JOURNAL REFERENCE

MEDLINE REFERENCE

JOURNAL

TITLE

AUTHORS TITLE

JOURNAL

ö

Gaps

ö

ö

Gaps

ö

22-SEP-1997

US-09-206-040-1.rge

윱 ò

```
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1382)
1 (bases 1 to 1382)
1 Lopato, S., Waigmann, E. and Barta, A.
Characterization of a novel arginine/serine-rich splicing factor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="splicing factor"
/db_xref="PID:e1169035"
/db_xref="PID:e2189035"
/db_xref="PID:g2589035"
/db_xref="PID:g2589035"
/db_xref="PID:g258035"
/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_xref="PID:g258035"

/db_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFDADNTRTRDLEKHFEPYGKIVNVRIRRNFAFIQYEAQEDATRALDASNNSKLMNKY
ISVEYAVKDDDARGNGHSPERRRDRSPERRRRSPSPYKRERGSPDYGRGASPVAA1 kn
ERTSPDYGRRRSPSPYKKSRRGSPEYGRDRRGNDSPRRRERVASPIKYSRSPNNKP!.\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSPNHSPFKKESPRNGVGEVESPIERRERSRSSPENGQVESPGSIGRRDSDGGYFGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I (bases I to 1493)

Kranz, H.D., Denekamp, M., Greco, R., Jin, H.-L., Leyva, A.,
Kranz, H.D., Penekamp, M., Greco, R., Jin, H.-L., Leyva, A.,
Smessner, R., Petroni, K., Urzainqui, A., Bevan, M., Martin, C.,
Smeekens, S., Toerenli, C., Paz. Arcs, J. and Weisshaar, B.
Towards functional characterisation of the members of the R2R3-MYB
                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (18-JUL-1996) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
Vienna, AUSTRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-OCT-1997) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Bukaryota, Viidiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnollophyta; eudicofyledons; Rosidae; Capparales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arubigopsis thaliana putative transcription factor (MYB92) mRNA, AR062916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Nov 2, 1997 this sequence version replaced gi:1707367.
Related sequence: T20696.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 24; Le
Pred. No. 5.65e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/variety="Columbia"
| Variety="taxon:3702"
| 146. .1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312
                                                                                                                                                                               Plant Cell 8 (12), 2255-2264 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPMOKSRSPRSPPADE'
274 c 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="RSp40"
146. .1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="RSp40"
                                                                                                                                                                                                                                                                                                                                                                                                                            ised by [3]
(bases 1 to 1382)
                                                                                                                                                                                                                                         (bases 1 to 1382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vienna, AUSTRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
                                                                                                                                                Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                Revised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases
Barta,A.
                                                                                                                                                                                                           97143875
                                                                                                                                                                                                                                                                     Barta, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="reversibly glycosylated polypeptide-3"
/db_xref="PID:g2645971"
/translation="MVEPANTVGLPVNPTPLLKDELDIVIPTIRNLDFLEMWRPFLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFSLREGVSTAVSHGLWLNIPDYDAPTOLVKPKERNTRYVDAVMTIPKGTLFPWCGMN
TEPDRELIEPRANTFGLMGOGPIGRYDDWMAGWCIKVICDHLGLGVKTGLPYIYHSKA
SNAPVNLKKEYKGIRMOEELIPFFQARLSKEAVTVQQCYIELSKMVKEKLSSLDPYF
DKLADAMVTWIEBAWDELNPPAASGKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHLIIVQDGDPSKKIHVPEGYDYELYNRNDINRILGPKASCISFKDSACRCFGYMVSK
KKYIFTIDDDCFVAKDPSGKAVNALEQHIKNLLCPSSPFFFWTLYDPYREGADFVRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATRSP40 1382 bp RNA PLN 31-OCT-1997
Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana Eukaryota; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Tracheophyta; seed plants; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis. (pases 1 to 1372) de Rocher, A., Keegstra, K. and Raikhel, N.V. Cloning and characterization of ARROPI. A reversibly autoglycosylated arabidopsis protein implicated in cell wall
                                                                                                                                                                                                    AF034255 1372 bp mRNA PLN 01-MAY-1998 Arabidopsis thaliana reversibly glycosylated polypeptide-3 (RGP) mRNA, complete cds. AF034255 92645970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1372)
Delgado, I., Wang, Z., de Rocher, A., Keegstra, K. and Raikhel, N.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-NOV-1997) Genetics, MSU-DOE-Plant Research Laboratory, 122 Plant Biology Building, East Lansing, MI 48824-1312, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          splicing factor.
thale cress.
Arabidopsis thaliana
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 25; Length 137
Pred. No. 5.65e-09;
"...marches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1372
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Physiol. 116 (4), 1339-1350 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GGAATTCCCGGGTCGACCCACGCGTCCG 39
                              GGAATTCCCGGGTCGACCCACGCGTCCG 30
                                                          99aattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="RGP3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /allele="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="RGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="RGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61. .1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                       thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92582640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98205072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSp40.
X99437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                               RESULT
```

ċ

Gaps

٩

g

ò

source

FEATURES

gene

CDS

JOURNAL MEDLINE REFERENCE

TITLE JOURNAL

AUTHORS

```
Submitted (14-JAN-1997) to the DDBJ/EMBL/GenBank databases. Hiroshi Takatsuji, National Institute of Agrobiological Resources, Plant. Physiology; 2-1-2 Kannondai, Tsukuba, Ibaraki 305, Japan (Tel:0298-38-838), Fax:0298-38-7417)
Location/Qualifiers
1. 1640
/organism="Petunia x hybrida"
/db_xref="taxon:4102"
/clone="Extracon:4102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"PEThy; 2PT3-1"
/db_xref-"PID: d1019856"
/db_xref-"PID: d1019856"
/db_xref-"PID: g1786138"
/db_xref-"PID: g1786138"
/db_xref-"PID: g1786138"
/db_xref-"MYDNSQUNEPSTVIHYCRVCRRGFNSAGALGGHMRSHGVGDHNK
NYGEDINEQRYMINNFRDKPRGOGKHSYNLRAMTNRLLGNRASEDRDKKSSMWPPNDR
GKYALDETLILSSMSSPGSSDLERSTRPYDAKEVYNGNDKDXXASREEEEDLANCLVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSNKSYVLSDNNEATYRAEEVEKGMFQCRACKKVFSSHQALGGHRASHKKVKGCYAAK
IXDDNDGNUDNNDNNDNDIDEDSISPSDITFHQESNEYGSQSPSSSSSSFSKRSRY
HQCSICHRVFSSGQALGGHRCHMLSSSLPENTFIPTFQETQYHTQEQGLFNKPMFTN
FDQFLDLNFPAQLGFRAEHELKLHNFFEHEGFRSYLQLWTDQINTNLHQNEKCKDST
EDLRREENYKDKEAKLSNLKDVNLDGGSSWLQVGIGPTPDIVATL"
                                                                                                                                                                                                                                                                               Seven zinc-finger transcription factors are expressed sequentially during the development of anthers and pollen in Petunia Unpublished (1997)

2 (basses 1 to 1640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1709)

Kilewer,S.A., Moore,J.T., Wade,L., Staudinger,J.L., Watson,M.A.,
Jones,S.A., McKee,D.D., Oliver,B.B., Willson,T.M.,
Zetterstron,R.H., Perlimann,T. and Lehmann,J.M.
An orphan nuclear receptor activated by pregnanes defines a novel
                                            gli86137
Lathor finder protein; ZPT3; transcription factor.
Petunia hybrida (cultivar:Mitchell diploid, lab_host:Escheriching coli, DH10B) stamen cDNA to mRNA, clone:ZPT3-1.
Petunia x hybrida
Eukaryotae; mitcochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Magnoliophyta; Magnoliophyta; Magnoliophyta; Solanaee; Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Cys(2) His(2) zinc finger protein, 3 fingers"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                             1 (sites)
Kobayashi,A., Sakamoto,A., Kubo,K., Rybka,Z., Kanno,Y. and
Takatsuji,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF031814 1709 bp mRNA ROD 08
Mus musculus pregnane X receptor mRNA, complete cds.
AF031814
92852328
      hybrida mRNA for PEThy; ZPT3-1, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 24; Length 164
Pred. No. 5.65e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host*"Escherichia coli, DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="stamen"
95. .1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 c
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
        Petunia h
AB000453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                    ORGANISM
        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                             ACCESSION
                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                    AUTHORS
                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative transcription factor"
/db_xxef="putative transcription factor"
/db_xxef="puto:g3941524"
/translation="MGRSPISDDSGLKKGPWTPDEDEKLVNYVQKHGHSSWRALPKLA
GLNRCGKSCRLRWTYLRPDIKRGRFSPDEEQTILNHSVLGNKWSTIANQLPGRTDN
EIKNFWTHLKKKLYQMGFDPWTHRPRTDIFSGLSQLMSLSSNLRGFVDLQQCPIDQ
EHTILKKGTRANKLQLPGYLLOPSSMNNNNNNDFDTLSLLNSTASFRSNWTSNN
LDLGFLGSYLQDFFSLRTLNSNREPSSYPPQNLDDNHFKFSTQRENTPNN
LDLGFLGSYLQDFFLSLRTLNSNREPSSYPPQNLDDNHFKFSTGRENTPNS
DPSSTTPAHVNDDLIFNQYGIEDVNSNITSSSGQESGASASAAWPDHLLDDSIFSDIP
                                                            Coases 1 to 1493)
Meissner,R., Jin,H.-L., Martin,C. and Bevan,M.
Direct Submission
Submitted (04-MAY-1998) Abt. Biochemie, MPI fur Zuchtungsforschung,
Carl-von-Linne-Weg 10, Koeln D-50829, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MYB92; R2R3-MYB factor family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 22; Length 158
Pred. No. 5.65e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN
                                                                                                                                                                                            1. .1493
/organism="Arabidopsis thaliana"
/cultivar="columbia"
/db_xref="taxon:3702"
/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 25; I
Pred. No. 5.65e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1581)
Voelker,T.Alols and Davies,H.Maelor.
Production of myristate in plant cells
Patent: US 5654495-A 1 05-AUG-1997;
Location/Qualifiers
1. .1581
    family from Arabidopsis thaliana
J. 16 (2), 263-276 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160018 1581 bp DNA
Sequence 1 from patent US 5654495.
160018
92478650
                                                                                                                                                                                                                                                                                                       /map="near marker ve033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 GGAATTCCCGGGTCGACCCACGCGTCCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"unknown"
356 c 410 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .1493
/gene="MYB92"
/allele="Col"
260. .1264
/gene="MYB92"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ัต
gene fami
Plant J.
99056848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB000453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown
```

10

RESULT

윱 ò

BASE COUNT

ORIGIN

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

FEATURES

REFERENCE

source

BASE COUNT

ORIGIN

11

RESULT LOCUS

29

요 ô

ö

```
cowpea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="pregnane X receptor"
//broduct="pregnane X receptor"
//db_xxef="pregnane X receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF071316 1779 bp mRNA ROD 03-SEP-1998
Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
AF071316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 1779)
Wei,N., Tsuge,T., Dohmae,N., Takio,K., Matsui,M. and Deng,X.-W.
Direct Submission
Submitted (11-JUN-1998) Department of Molecular, Cellular, and
Developmental Biology, Yale University, 165 Prospect Street, New
Haven, CT 06511, USA
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wei, N., Tsuge, T., Serino, G., Dohmae, N., Takio, K., Matsui, M. and Deng, X.W.
The COP9 complex is conserved between plants and mammals and is related to the 26S proteasome regulatory complex
Curr. Biol. 8 (16), 919-922 (1998)
                                                                                        Clases 1 to 1709)
Kliewer,S.A., Moore,J.T., Wade,L., Staudinger,J.L., Watson,M.A., Jones,S.A., McKee,D.D., Oliver,B.B., Willson,T.M., Zetterstrom,R.H., Perlmann,T. and Lehmann,J.M.
Direct Submission
Submitted (29-0CT-1997) Department of Molecular Endocrinology, Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pregnane-activated nuclear receptor"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 29; Length 1709; 5.65e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/tissue_type="liver"
151. :1446
/function="steroid signaling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BLKS"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           steroid signaling pathway
Cell 92 (1), 73-82 (1998)
98149345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="COPS7a"
159. 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="COPS7a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93309173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                     MEDLINE
                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURES
                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
/translation="MAASNASTAD"
//translation="MAASNASTAD"
//translation="MAASNASTAD"
//translation="MAASNASTAD"
//translation="MAASNASTAD"
//translation="MAASNASTAD"
//translaterricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerricelerrice
Anotes" subunit 7a is a component of the COP9 complex which contains a total of 8 distinct subunits, similar to the JAB1-containing signal come; the plant COP9 complex functions as a repressor of photomorphogenesis"
                                                                                                                                                                                                                                                                                                                          /product="COP9 complex subunit 7a"
//d=xref="ID193309174"
//d=xref="ID193309174"
//tanslation="MASAEWYNTONDEOFILLAKSAKGAALATLIHOVLEAPEVYYV***-
ELLDMPNYBELAESDFASTFRILITVFAYGTYADYLAEARNLPPITDAOKNKLRHI.SVV
TIAAKWYCIPTYALLERLARNYADEDLYERSYADVLRGSTDORNOKESUDYSTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSYTONDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTSTANDEOUTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="phosphoribosylpyrophosphate amidotransferase"
/db_xref="PID:93243256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           רוטר 23-JUN-1998
Vigna unguiculata phosphoribosylpyrophosphate amidotransferase
(purl) mRNA, complete cds.
AF071862
93243255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.0%; Score 28; DB 29; I
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Vigna unguiculata"
/strain="Vita 3"
/db_xref="taxon:3917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="root nodule"
/dev_stage="day 22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="purl"
/EC_number="2.4.2.14"
/note="PRAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 GGAATICCCGGGTCGACCCACGCGTCCG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      470 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="purl-10"
                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pur1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="|
45. .17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
```

```
/product="3-ketoacy1-ACP synthase"
/db_xref="PID:g3800747"
/db_xref="PID:g3800747"
/db_xref="PID:g3800747"
/translation="WPAASSLAASPLCTWLLAACMSTSFHPSDPLPPSISSPRRRLSR
RILISOCAPLPSASSALAGSEFUTVTSYLAGFEPCHDYYTSASLFGSPIRTTRRHR
RLNRASPSREAMAVALQPEQEVTTKKRPSIKQRRVYVTGMGVYTPLGHDPDVFYNNLL
DGTSCISEIETPCAGPFTRIAGEIKSFSTDGMVAPKJCKRMDRFMLYMLTAGKKALT
DGGTTEDVMKELDKRKGGVIGSAMGGWVFNDAIEALRISYKKMNPFCVPATVNMG
SAMLAMDLGMWGPNYSITSNFCIMNCTMNAANHINGBADVMLCGGSDAVIIPIGMG
GFVACRALSORNSDPTKASRPWDSNRDGFVMGEGAGVLLLEELEHAKKRGATIYAFFL
GGSFTCDATHWTBELTVNSTKSMIGHLLGARGGVSREDVNYINHATSTPAGDIKEYQ
ALHGFGQNRELKVNSTKSMIGHLLGAAGGVEAVSVVQAIRTGWHHNINLENPDEGV
DTKLLVGPKRERLNVRTGSNSFGFGGHNSSILFAPYI"

1 a 563 c 537 g 637 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 2351)
Dehesh.K., Edwards.P., Fillatti.J., Slabaugh.M. and Byrne.J.
KAS IV: a 3-ketoacyl-ACP synthase from Cuphea sp. is a medium chain specific condensing enzyme
Plant J. 15 (3), 383-390 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (20-APR-1998) Oils division, Calgene, 1920 Fifth Street,
Davis, CA 9561, USA
Location/Qualifiers
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                          AF060518 2351 bp mRNA PLN 28-OCT-1998 Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                     Cuphea pulcherrima.
Cuphea pulcherrima
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnollophyta; eudicotyledons; Rosidae; Myrtales; Lythraceae;
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 25; Length 2351;
Pred. No. 5.65e-09;
0; Mismatches 0; Indel's
                                                        Length 2111;
                                                                                           0; Indels
                                                      Score 28; DB 25; I
Pred. No. 5.65e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Cuphea pulcherrima"
/db_xref="taxon:83566"
1. 2351
/gene="Kas4"
217. .1857
 514 t
                                                                                           0; Mismatches
                                                                                                                            8 GGAATTCCCGGGTCGACCCACGCGTCCG 35
                                                                                                                                                    29 ggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GGAATTCCCGGGTCGACCCACGCGTCCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217. .1857
/gene="Kas4"
/note="KAS IV"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2351)
Dehesh, K.
                                                    Ouery Match 6.0%;
Best Local Similarity 100.0%;
Matches 28; Conservative
 υ
 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 a
497 a
                                                                                                                                                                                                                                                                                   cds.
AF060518
g3800746
                                                        Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                            RESULT
                                                                                                                                g
                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
```

Search completed: Mon Mar 8 23:10:00 1999 Job time : 1741 secs.

THIS PAGE BLANK (USPTO)

*		(TM)
'_	' ' 	
]
'- -		<u>'</u> <u>-</u>
'\ 	<u>}}</u>	
<u>_</u>		

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- n.a. database search, using Smith-Waterman algorithm n.a. MPsrch_nn

Mon Mar 8 21:15:30 1999; MasPar time 746.68 Seconds 1484.353 Million cell updates/sec Run on:

not generated. Tabular output

>US-09-206-040-1 (1-469) from US09206040A.seq 465 Title: Description: Perfect Score: N.A. Sequence: Comp:

1 ttaacttgcagcgnccaggt........gatgatacattgaagatnnt 469 aattgaacgtcgcnggtcca.......tactatgtaacttctanna

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD 602357 seqs, 1181590623 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

1:em_ba 2:em_fun 3:em_htg 4:em_huml 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_un 15:em_vi
genbank110 emb157 Database:

16:9b_bal 17:9b_ba2 18:9b_htg 19:9b_in 20:9b_om 21:9b_ov 22:9b_pat 23:9b_ph 24:9b_pll 25:9b_pl2 26:9b_prl 27:9b_pr2 28:9b_pr3 29:9b_ro 30:9b_st 31:9b_st 32:9b_sy 33:9b_un 34:9b_vi

Database:

Mean 10.123; Variance 4.816; scale 2.102 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		•					
Result No.	Score	Query Match	å Query Match Length DB	DB	ΩI	Description	Pred. No.
-	45	9.7	7218	22	166494	Sequence 14 from paten	2.62e-14
7	38	8.2	367	31	HSRSTS367	H.sapiens STS, 367bp,	2.19e-09
m	38	8.2	1382	24	ATRSP40	Arabidopsis thaliana m	2.19e-09
4	38	8.2	1493	25	AF062916	Arabidopsis thaliana p	2.19e-09
3	38	8.3	1581	22	160018	Sequence 1 from patent	2.19e-09
9	38	8.2	2351	25	AF060518	Cuphea pulcherrima 3-k	
د ۲	37	8.0	965	22	AR024229	Sequence 22 from paten	
œ	37	8.0	10772	13	AF012089	Drosophila melanogaste	1.05e-08
თ ს	37	8.0	10772	19	AF012089	Drosophila melanogaste	1.05e-08
10	37	8.0	74371	27	AC005369	Homo sapiens chromosom	-
11	36	7.7	3410	56	HSU27699	Human pephBGT-1 betain	
c 12	36	7.7	7218	22	166494	Sequence 14 from paten	5.00e-08
13	36	7.7	8665	28	HSU86136	Human telomerase-assoc	

4.850-0: 4.850-0: 4.858-0:		9.37e-05 4.00e-04			6.83e-03	6.83e-03		2.72e-02	2.72e-02	2.72e-02	2.72e-02	2.72e-92	2.72e-v2	2.72e-0	2.72e-02	2.72e-02	2.72e-02	2.72e-02	1.06e-01	1.06e-01	1.06e-01	1.06e-01	1.06e-01	1.06e-01
Human tazarotene-induc Petunia hybrida mRNA f Homo sapiens monocyte/	Arabidopsis thaliana r Vigna unguiculata phos	Mus musculus COP9 comp Homo sapiens mRNA for	Sequence 5 from patent		Mus musculus Nmi mRNA,	Mus musculus pregnane Homo sapiens Chromosom	Sequence 1 from Patent	ß	human STS SHGC-12120 c	Sequence 1 from patent	HIV-1 strain W32 from	Arabidopsis thaliana m	HIV-1 strain H35 from	X.laevis mRNA for Na, K	M.musculus mRNA for co	Oryctolagus cuniculus	Cloning vector pSVSpor	Cloning vector pSport1	Sequence 6 from Patent	human STS SHGC-12116 c	Sequence 22 from paten	Homo sapiens chromosom	*** SEQUENCING IN PROG	Homo sapiens Chromosom
HSU77594 AB000453 AF004231	AF034255 AF071862	AF071316 AB016247	128278 HSXS16	AB010946	AF019249	HUAC004787	A62989	128278	G11956	AR023813	HIVU84881	ATRNABIND	HIVU84883	XLNAKATP	MMCARHOM	OCU36790	PSVSPORT	PSPORT1	A62994	G11955	AR024229	AC005369	AB018117	HUAC004787
224	25	28	22	24	53	22	22	22	31	22	34	25	34	21	53	20	32	33	22	31	22	27	18	23
770 1640 2879 73428	1372	1779	215	1009	1214	216021	9	215	400	538	1271	1291	1321	1500	1669	2344	3160	4109	30	400	965	74371		216021
	10.0		00		0.0		•		٠			•		٠.					9			9	•	9
<i></i>	99	ω ω	ωw	Φ	9	oυ	w	w	S	ഗ	LID.	u	L)	ın	ഗ	ហ	L)	n	വ	'n	'n	S	'n	LC)
	3 3 3	30	28	28	5 8	7 8	27	27	27	27	27	27	27	27	27	27	27	27	26	26	56	56	56	56
14 15 16	18	220	22	24	22	270	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5
c)							U			υ		U					U				υ		ပ

ALIGNMENTS

			ő				
997				1225 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	1344	1345 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	
23-DEC-1997			0; Gaps	YYY ::	YYY : agt	YYY : atg	
ag-			.; .;	YYY : aat	YYY :: tcg	YYY :::	
23		ιo.	8;	YYY : : tac	YYY 99a	YYY :: atc	
	ë.	her	72 els	YYY : ata	чүү	YYY	
· .	ınte	368 others	igth	YYY :::	YYY	YYY	
PAT	9	368	Length 7218; ; 3; Indels	YYY ::	YYY : ;	: :9cg	
	er, E		14,	XXXX ::::	ryyy : aatç	 	
	1kne 97;	9 ب	DB 22; 2.62e-14 tches 8	ryy ::::	YYY	YYY) : :	'n
036	Fa.	1929 t	2. atc	YYY ::: ttc	YYY ::: ttc	YYY :: ccg	143
567	and SEP s		45; No.	YYY : caa	xxx : gat	YYY :: atc	χĊ
DNA	F. 23-	10 VI	Score 45; DB 22; Length 72: Pred. No. 2.62e-14; 127; Mismatches 83; Indels	YYY ::	YYYY ::	rrrr ::	XXX
ent.	Jer, 71ru 14	148 148	Scc Pre	rryy :::	rryy ::::::	rryy : ataa	CYYY
166494 7218 bp DNA Sequence 14 from patent US 5670367 166494 92724471 Unknown.	Unclassified. 1 (bases 1 to 7218) Dorner, F., Scheiflinger, F. and Falkner, F. Gunter. Recombinant fowlpox virus Patent: US 5670367-A 14 23-SEP-1997; Location/Qualifiers 17218	∕organism≕"unknown" 1491 c 1486 g		rrr:	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	YYY) : gcae	YYY
218 om	72 e1f w1p 036 100,	nts 91	9.7%; similarity 0.5%; 1; Conservative	YYY :: tcg	YYY :: ttg	YYY : tgg	YXX
fr	led. 1 to 72 , Scheif nt fowlp 5 567036 Location 17218	rga 14	rva	YYY :: cta	YYY	YYY : gta	XXX
14	is 1	୧	itty onse	XXX : : JCat	YYY :	Y Y Y	XXX
94 94 94 71 94 94 94 94 94	er, E	1944	Llar	ryyy ::::	ryyy :::: gtto	rrry	CXXX
166494 Sequence 166494 92724471 Unknown.	Unclassified. 1 (bassi 1 to 7218) Dorner,F., Scheifiln Recombinant fowlpox Patent: US 5670367-A Location/Qu 1. 7218	Ä	Sim:	YYY : : tgc1	YYY ::	YYY	KKK
н			tch al	YYY :::	YYY : ata	YYY : :	XXX
RESULT LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM	ENCE HORS LE RNAL RES SOUTCE	BASE COUNT ORIGIN	Query Match Best Local Similarity Matches 1; Conser	225 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	1285 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	345 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	1405 YYYYXYYYYYYYYYYYYYYYYYYYYYYY 1435
RESULT LOCUS DEFINITIO ACCESSION NID KEYWORDS SOURCE ORGANISI	REFERENCE AUTHORS TITLE JOURNAL FEATURES	SIZ SIZ	Query Ma Best Loc Matches	7 7	7	H	14
LOCUS LOCUS DEFINI ACCESS: NID NID KEYWORI SOURCE ORGAI	REFI A(T: C(BASE CO	ÕÄÄ	Dp Oy	g &	g y	g

~

Page

NID

ò

```
complete cds.
AF062916
g3941523
 by [3]
                             Barta, A.
 Revised
                                                                                                                                                                                                                                                                                                                                                                                                                                                            406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
REMARK
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; viridiplantae; Charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Magnoliophyta; Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1382)

Lopato, S., Waigmann, E. and Barta, A.

Characterization of a novel arginine/serine-rich splicing factor in
                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-SEP-1996) A.B. McKie, ICRF Molecular Pathology Group,
8th Pioor, MRC Cyclotron Bldg, Hammersmith Hosp, Ducane Road,
London, W12 ONN, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATRSP40 1382 bp RNA PLN 31-OCT-1997
Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (18-JUL-1996) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
Vienna, AUSTRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                  Alu-polymerase chain reaction genomic fingerprinting technique identifies multiple genetic loci associated with pancreatic tumourigenesis
                                                                                                                                                     Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 367)
MCKie,A.B. Iwamura,T., Leung,H.Y., Hollingsworth,M.A. and
Lemoine,N.R.
                                                             16-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                  Genes Chromosomes Cancer 18 (1), 30-41 (1997)
                                                  HSRSTS367 367 bp RNA STS
H.sapiens STS, 367bp, sequence tagged site.
Y07966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 31;
Pred. No. 2.19e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ىد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Cell 8 (12), 2255-2264 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .367
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetal"
/tissue_type="brain"
/lab_host="E.coli"
/chromosome="17"
330 ttcgccactttcgcttctatctacgtcgctg 360
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                          STS; sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="p13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%;
ilarity 95.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splicing factor.
thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1382)
                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 367)
McKie, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .>367
146 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
                                                                                                         g1552329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q2582640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97143875
                                                                                                                                                                                                                                                                                                                97147122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barta, A.
                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
                                                                       DEFINITION
                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STS
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                  TITLE
                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

8 ò

```
/product="spliting factor"
//product="spliting factor"
//db_xref="pip:al16903s"
//db_xref="pip:al26903s"
//db_xref="pip:al26903s"
//db_xref="pip:ag2582641"
//translation="mkrefconferyDarRegoleRicsesSanReskTifvU
BrDADMIRATADLEKHFEPYGKINVNTIRNFAFIQYEQGGSRRSSSSNRFSKTLFVI
BRDADMIRATROLEKHFEPYGKINVNTIRNFAFIQYEQGDATRALDASNNSKLMINV
ISVEYANKDDARGOHSPERRRDRSPERRRSPSPYKREKGSPDYCRGASPVANIKA
MSPNHSPFKKESPRGSPERRRSPSPYKKESRRNKEH;
MSPNHSPFKKESPRGVGEVESPIERRERSRSPPRGSPGGSTGRRDSDGGYWANK
SPNMSRSPRRSPDGGVEVENDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis.

(bases 1 to 1493),
Kranz, H.D., Denkamp, M., Greco, R., Jin, H.-L., Leyva, A.,
Meissner, R., Denkamp, M., Graco, R., Jin, H.-L., Leyva, A.,
Smeekens, S., Tonelli, C., Paz-Ares, J. and Weisshaar, B.
Towards functional characterisation of the members of the R2R3-MYB Plant J. 16 (2), 263-276 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-MAY-1998) Abt. Biochemie, MPI fur Zuchtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany Location/Qualifiers
                                                   Direct Submission
Submitted (30-007-1997) A. Barta, Institut of Biochemistry,
Submitted (30-007-1997) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1038
Vienna, AUGYRIA
On Nov 2, 1997 this sequence version replaced gi:1707367.
Related sequence: T20696.
Location/Qualifiers
1. 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnollophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF062916 1493 bp mRNA PLN 02-DEC-1998
Arabidopsis thaliana putative transcription factor (MYB92) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 24; Length 1382;
Pred. No. 2.19e-09;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1493)
Meissner, R., Jin, H.-L., Martin, C. and Bevan, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 caggtancggtcaggaattcccgggtcgacccacgcgtccg 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Arabidopsis thaliana"
/cultyar-"Columbia"
/db_xref-"taxon:3702"
/chromosome-"v"
                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
//variety="Columbia"
                                                                                                                                                                                                                                                                                                                                             /db_xref-"taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPMQKSRSPRSPPADE
274 c 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="RSp40"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                          /gene="RSp40"
146. .1198
(bases 1 to 1382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.2%;
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 .1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1493
```

```
RLNRASPSREAMAVALQPEQEVTTKKKPSIKORRVVVTGMGVVTPLGHDPDVFYNNLL
DGTSGISEIETEPDCAQPPTRIAGEIEKSSTDGWPAFKLSKRNDKFMLYHTAGKKALT
DGGITEDVMKELDKRKGVLIGSAMGGMKVPRDAIEALRISYKMNPFCVPFATTNMG
SAMLAMDLGWMGPNYSISTACAISNFCIMNAANHIIRGEADVMLCGGSDAVIIPIGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFVACRALSQRNSDPTKASRPWDSNRDGFVWGEGAGVLLEELEHAKKRGATITAEFL
GGSFTCDAYHMTEHFDGAGVILCTEKALAGSGVSREDVNYINAHATSTPAGDIKEYO
ALIHCFGQNRELKVNSTKSMIGHLLGAAGGVEAVSVVQAIRTGWIHPNINLENPDEGV
DTKLLVGPKKRLLWYGLSNSFGFGGHNSSILFAPYI
563 c 537 g 637 t 1 others
                                                                                                                                                                                                                                                                                                                                  /product-"3-ketoacy1-ACP synthase"
//bc/xref-"piD:g380/A1/"
//translation-"MRAASSLLASPLCTWLLAACMSTSFHPSDPLPPSISSPRRLSR
RRILSQCAPLPSASSALRGSSFHTLVTSYLACFEPCHDYYTSASLFGSRPIRTTRRHR
                                                                                              Direct Submission
Submitted (20-APR-1998) Oils division, Calgene, 1920 Fifth Street,
Davis, CA 9561, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 HTVHVSGGVRSTSTCTASDYTTSYWGWVRGRGWGDYGGGYTNYNGKRGRVTMADTSSNSR 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 ctctgcgtcctgccacagccttccagcgacgtagatagaa-gcgaaagtggcgaacatgg 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 965)
Wallace, T. Paul, Harris, W. J., Carr, F. J., Old, L. J., Welt, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   844 SSVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHTVKDMTSSSSAS 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 CAGGIACCGGICCGGAATICCCGGGICGACCCACGCGICCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant human anti-Lewis b antibodies
Patent: US 5795961-A 22 18-AUG-1998;
Location/Qualiflers
1. 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 38; DB 25; 1
larity 95.1%; Pred. No. 2.19e-09;
Conservative 0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 22;
Pred. No. 1.05e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:83566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR024229 965 bp DNA
Sequence 22 from patent US 5795961.
AR024229
33977523
specific condensing enzyme
Plant J. 15 (3), 383-390 (1998)
98422743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
170 c 226 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :: -:::
                                                                                                                                                                                                                                                                                                /note="KAS IV"
                                                                                                                                                                                                                                                                            /gene="Kas4"
                                                                                                                                                                                                                                              /gene="Kas4"
                                                             2 (bases 1 to 2351)
Dehesh, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 20.2%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitamura, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S:
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ^
                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                 MEDLINE
REFERENCE
                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                    JOURNAL
                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                /product="putative transcription factor"
/db_xref="putative transcription factor"
/db_xref="puton="MGRSP150DSGLKGPWTPDEDEKLVNYVQKHGHSSWRALDKLA
/translation="MGRSPTSDDSGLKGPWTPDEDEKLVNYVQKHGHSSWRALDKLA
GLNRCGKSCRLKWTYLRPDIKRGRESPDEGTILNHSVLGNKWSTIANQLPGRTDN
EIKNFWTHLKKKLIOMGFDPWTHRPRTDIFSGLSQLMSLSSNLRGFVDLQQCFPIDG
EHTILKLGTEARAKLQFFQFLQPSSWNNVNRPDFDTLSLLNSIASFRETSNWTTSNN
LDLGFLGSYLQDFFARSLKTLNSNWEPSSYPPQNLDDNHFKFSTQRENLPVSPIWLS
DPSSTTPAHVNDDLIFNOYGIEDVNSNITSSSGQESGASASAAWPDHLLDDSIFSDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T (bases 1 to 2351)
Dehesh,K., Edwards,P., Fillatti,J., Slabaugh,M. and Byrne,J.
KAS IV: a 3-ketoacyl-ACP synthase from Cuphea sp. is a medium chain
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1998
mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; Myrtales; Lythraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                /note="MYB92; R2R3-MYB factor family member"
                                                                                                                                                                                                                                                                                                                                                                     Length 1493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1581;
                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 25; Length 149
Pred. No. 2.19e-09;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF060518 2351 bp mRNA PLN Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 CAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 22; Le
Pred. No. 2.19e-09;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1581)
Voelker,T.Alois and Davies,H.Maelor.
Production of myristate in plant cells
Patent: US 5654495-A 1 05-AUG-1997;
                                                                                                                                                                                                                                                                                                               412 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150118 1581 bp DNA
Sequence 1 from patent US 5654495.
160018
           /map="near marker ve033"
1. .1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
356 c 410 g
                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 290
                                                                                                                                     /codon_start=1
                                                                                                  /gene="MYB92"
                                              'gene="MYB92"
                                                              /allele="Col"
                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.2%;
Best Local Similarity 95.1%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 8.2%;
Local Similarity 95.1%;
les 39; Conservative
                                                                                 .1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cuphea pulcherrima.
Cuphea pulcherrima
                                                                                                                                                                                                                                                                                                                 321 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified
                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF060518
g3800746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92478650
                                                                                                                                                                                                                                                                                                                 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cuphea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                 COS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

ö

Gaps

ö

Indels

Length 2351;

04-DEC-1998

PAT

26

Length 965

Indels

172 others

```
2282 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="CP1"
872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   872. .1000
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number=1
1001. .2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watch 8.0%;
Local Similarity 19.6%;
hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     2357 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92305220
                                                                                                                                                                                                                                                                                                                                                                                                                     2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="cysteine proteinase-1"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305221"
/db_xref="PID:92305275"
/db_xref="PID:9230527
AF012089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089
                                                                                                                                                                                                                    fruit fly.

Drosophila melanogaster

Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;

Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;

Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.

( bases 4546 to 4553)

Gray Y. H., Tanaka, M.M. and Sved, J. A.

P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
3 (bases 1 to 10772)
3 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University Sydney, Biology Al2, Sydney University, NSW 2006, Australia Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila
melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref=taxon:7227"
join (872. 1000,2310. 2426,6476. 6690,6751. 7707)
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(2328. .2426,6476. .6690,6751. .7462)
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2427. .6475
/gene="CP1"
4546. .4553
/gene="CP1"
/note="insertion site of P{CaSpeR}(50C)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="cysteine protease"
872. .7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics 144 (4), 1601-1610 (1996)
97132596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /citation=[1]
6476. .6690
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=1
1001. .2309
/gene="CP1"
2310. .2426
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6691. .6750
/gene="CP1"
6751. .7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="CP1"
872. .1000
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 element insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                       ω
                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
join(<8110..9300,9370..>9532)
/product"phenylalanyl tRNA synthetase"
join(8110..9300,9370..>9532)
/forde="potential orf"
/codon_start=1
/codon_start=1
/codon_start=1
/product="phenylalanyl tRNA synthetase"
/product="phenylalanyl tRNA synthetase"
/db_xref="PID:9230222"
/translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
TDGATWYDFRILSYVGANKHLQTDHPLSITRQRIVFYTGARRNQRGRPLEYSYDQMN
PVYTVQQNFDNLLIPADHVSRQKSDCYXINQQHLLRAHTTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVHADHDANYLLYTROKLERNFOGLELFEETWSGTLADFKLILPHP
SSWTRPNSPATRRYKLMFHENGNSGVHQSIGTARDFCARFANVLFDIPDIREFWSNDS
GFLSQFSERCLHNLENKYRESHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLYRSVNG
GFLSQFSERCLHNLENKYREPSHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLYRSVNG
DNWEQISLVDKFKHPRTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF012089 10772 bp DNA 10702 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray, Y.H., Tanaka, M.M. and Sved, J.A. P-element induced recombination in Drosophila melanogaster: hybrid element insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Submitsed (30-JUN-1997) school of Biological Sciences, University,
of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
1. . 10772
/ Organism="Drosophila melanogaster"
/ Ab_xref="taxon:7227"
join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
/ gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1723 WMWKMYWTSRTTTTSAMMMYTWSTWTKYWWAYAWMKMWWTRTWARMAWASWARWKWKTS 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 10772)
Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
Structure of the cysteine proteinase (CP1) gene of Drosophila metanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae, mitochondrial eukaryotes, Metazoa, Arthropoda,
Tracheata, Hexapoda, Insecta, Pterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
1 (bases 4546 to 4553)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1783 AAAAYSAWR-KMWKWWAYRAMKKTWMWAAWKWRWKAAWWTWRWWYMT 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 19; Length 107
Pred. No. 1.05e-08;
56; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || |::|:: :: :: |::| :| :| :: :: :: |::| :: :| 204 aatatcataatcgttcataagattgcatttgcatttgcattgatttcaaaaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="cysteine protease"
872. 7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3046 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics 144 (4), 1601-1610 (1996)
97132596
              mRNA
```

```
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.N., Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H., Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                              Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
                                                                                                                                                                                                                                                                                                                                          Unpublished

(Leases 1 to 74371)

(Leases 1 to 74371)

(Minerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Bondoc, M., Miguel, T., Pitluck, S., Pollard, M., Rojeski, H., Subramalan, S. and Martin, C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="65% 6 69% protein identity GenPept:U22377" 3431. .3724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7830. .8185)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_type=tandem
/rpt_unit=GT
join(3246. .3410,3721. .3828)
/standard_name="kEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9070. .9387
/rpt_family="Alu"
complement(9740. .9845)
/rpt_family="MER42"
complement(10440. .11015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .11015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/db_xref="taxon:9606"
/map="5q"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOE Joint Genome Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Chromosome="5"
/note="12BNL H175"
893. 1030
/rpt_family="Alu"
2295. 2438
/rpt_family="Alu"
22818. 2859
/note="(GT)21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3431. .3724
/rpt_family="Alu"
3707. 2772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4366. .4661
/rpt_family="Alu"
5327. .5602
/rpt_family="Alu"
6586. .6956
/rpt_family="L1"
6647. .6684
/note="(CA)19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu" complement(7830. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3258. .8503
rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
11950. .12250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
12057. 12057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_type-tandem
/rpt_unit-CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="11953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3707. .3728
/note="(A)22"
                                                                                                                                                                                                        2 (bases 1 to 74371)
Ricke, D.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_unit=A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .74371
                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
   REFERENCE
AUTHORS
                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                /product="cysteine proteinase-1"
/db_xref="PiD:g2305221"
/db_xref="PiD:g2305221"
/db_xref="PiD:g2305221"
/db_xref="PiD:g2305221"
/db_xref="PiD:g2305221"
/db_xref="PiD:g2305221"
/db_xref="PiD:g2305221"
/db_xref="PiD:g230521"
/db_xref="PiD:g230521"
/db_xref="PiD:g2525"
/db_xref="PiD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"phenylalanyl trna synthetase"
/db_xref="PiD:92305222"
/db_xref="PiD:9230522"
/db_xref="PiD:9230522"
/db_xref="PiD:9230522"
/db_xref="PiD:9230522"
/db_xref="Millengramming."

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSWTKPNSPATRRAKLMEHENKHVLVGLTKDLFGPRIKYRWDTYFPFTQPSWELEI
YFKDWWLEVLGCGIMRHEILORSGVHQOSIGYAFGVGLERLAMLLEDIDDTRLFWSNDS
GFLSQFSEKDLHNLFRYKPISHYPQCYNDLSFWLPQDIEVDAGFSPNDFYDLYRGVAG
DMYGOISLVDKFKHPRTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFWVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete sequence. Accobs369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1691 AKRWWYWAWTITMWKWWWITWKWAMMKIYRIWWWKMYW-ISRITITSAMWMYTWSIWI 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10772;
                                                                                                                                     join(2328. .2426,6476. .6690,6751. .7462)
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 19; Length 107
Pred. No. 1.05e-08;
55; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1750 KYWWAYAWMKMWWTRTWARMAWASWARWKWKTSAAAAYSAWRKMWKW 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="insertion site of P{CaSpeR}(50C)" /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="phenylalany1 tRNA synthetase"
join(8110. 9300,9370. >9532)
/note="potential orf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .>9532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3046 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9300,9370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2282 g
                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSYPLV"
2427. .6475
/gene="CP1"
4546. .4553
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6691. .6750
/gene="CP1"
6751. .7707
                                   2310. .2426
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6751 .7707
/gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6476. .6690
/gene="CP1"
'gene="CP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(<8110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 8.0%;
Best Local Similarity 20.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'number-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
```

셤 g 셤 g

```
/rpt_type=tandem
/rpt_unit=A
/rpt_unit=A
28712. 28930
/rpt_family="MER20"
complement(28769. .28838)
/note="GRAIL 2 excellent exon, frame 0"
/rpt_family="Alu"
                                                                                                               /rpt_family="tl"
14175. 14470
Tpt_family="Alu"
complement(14006. .15259)
/standard_name="possible repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22321. .22457
/rpt_family="Alu"
complement(22638. .22981)
/standard_name="possible repeat"
23022. .23326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (24639. .24694)
/rpt_family="MER42"
complement (25349. .25713)
/rpt_family="Alu"
complement (25727. .26471)
                                                                                                                                                                                                                                                                                                              complement(16993. .17085)
/rpt_family="MER42"
complement(17678. .18276)
/rpt_family="Alu"
19305. .19583
/rpt_family="Alu"
19914. .19945
/note="(GTT1)8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alu"
27191. .27477
                                                                                                                                                                                                                                                                                  complement(16675. .16977)
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(19943. .20222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //rpt_family="Alu"
27774. 28057
/rpt_family="Alu"
28040. 28066
/note="(A)27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
21202. 21496
/rpt_family="Alu"
21736. .22035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alu"
22017. .22038
/note="(A)22"
/rpt_type=tandem
/rpt_unit=A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
23473. 23761
/rpt_family="Alu"
23744. 23767
/note="(A)24"
/rpt_unit=A
12365. .12645
/rpt_family="Alu"
13727. .13750
/note="(AC)12"
                                                                                                                                                                                                           /rpt_family="Alu"
.6671. 16690
'note="(T)20"
                                                                                                                                                                                                                                                                                                                                                                                                                                       'rpt_type=tandem
'rpt_unit=GTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_type=tandem
/rpt_unit=A
                                                                                                                                                                                                                                                         rpt_type=tandem
                                                                          rpt_type=tandem
                                                                                                       .14024
                                                                                        7rpt_unit=AC
                                                                                                                                                                                                                                                                      'rpt_unit-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                 repeat_region
                                              repeat_region
                                                                                                       repeat_region
                                                                                                                                     repeat_region
                                                                                                                                                                  repeat_region
                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
```

1

```
Db 15951 MWMTCKSSKCWCWSYRMRMKCYSCSYCYCSSGKKYWCRCSMYWYTCYYSYKYYWSMSYCT 16010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 16011 CTSWG-WRWMWSKGRSWMYASRSGCSCSCSMCMMCRCSCMSWKWWWTTTTTKTRTWTTT 16069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: | ::::|: : ::::|: : :|::| ::: | :::: | 340 281 cagtatgggcaataatcgatcccgcattcccgcgctcctcatctccatcttccatcttcatctt 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 27; Length 74371;
Pred. No. 1.05e-08;
72; Mismatches 50; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSU27699 3410 bp mRNA PRI 09-FEB-1991
Human pephBGT-1 betaine-GABA transporter mRNA, complete cds.
U27699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
join(29485. .29559,29598. .29779)
/note="95% identity dbsTs:G14522 (SHGC-11312)"
29495. .29976
                                             /standard_name="A1027942"
/note="100% identity EST ov84a10.x1"
/note="6RALL 2 excellent exon, frame 2"
complement(30682.30733)
/rpct_anily="Mrrs"
/note="6RALL 2 excellent exon, frame 1"
/note="6RALL 2 excellent exon, frame 2"
32388 32488
                                                                                                                                                                                                                                                                                                                                                                 /note-"GRAIL 2 excellent exon, frame 2" complement(35238. 35331) /note-"GRAIL 2 excellent exon, frame 1"
                                                                                                                                                                                                                                                    32617. .32908
7rpt_family="Alu"
32977. .33088
/rpt_family="MLT1"
complement(33670. .33785)
/rpt_family="Alu"
complement(34021. .34144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16070 WKWRKAGASASRGKSKCRCMSYGK 16093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: remainder of annotations omitted.
                                                                                                                                                                                                                                     "MLT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 caaagagctcgataggatcactgg 424
                                                                                                                                                                                                                            /rpt_family=",32617,32617
                                                                                                                                                                                                                                                  .32908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.0%;
Best Local Similarity 14.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9881474
                                                                                                                     repeat_region
                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
      misc_feature
                                     misc_feature
                                                                                    misc_feature
                                                                                                                                                     misc_feature
                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
13
                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                            g
                                                                           g
L (bases 1 to 3410)
Rasola, A., Galietta, L.J., Barone, V., Romeo, G. and Bagnasco, S.
Molecular cloning and functional characterization of a GABA/betaine
transporter from human kidney
FEBS Lett. 373 (3), 229-233 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLKDPQVWMDAGTQIFFSFAICQGCLTALGSYNKYHNNCYKDCIALCFLNSATSFVAG
FVVFSILGFMSQEQGVPISEVAESGPGLAFIAFPKAVTWMPLSQLWSCLFFIMLIFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLATFLFSLSKYTPLKYNNVYVYPPWGYSIGWFLALSSMVCVPLFVVITLKTRGPFR
KRLRHVITPDSSLPQPKQHPCLDGSAGRNFGPSPTREGLIAGEKETHL"
                                                                                                                                                                                                                                                                                                                                                                    GSVTAWRKICPLFQGIGLASVVIESYLNVYYIIILAWALFYLFSSFTSELPWTTCNNF
WNTEHCTDFLNHSGAGTVTPFENFTSPVMEFWERRVLGITSGIHDLGSLRWELALCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAWVICYFCIWKGVKSTGKVVYFTATFPYLMLVILLIRGVTLPGAYQGIIYYLKPDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSQFVCVECLVTASIDMFPRQLRKSGRRELLILTIAVMCYLIGLFLVTEGGMYIFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDYYASSGICLLFLSLFEVVCISWVYGADRFYDNIEDMIGYRPWPLVKISWLFLTPGL
                                                                                                                                   Rasola,A.
Direct Submission
Submitted (25-MAY-1995) Andrea Rasola, Laboratorio Di Genetica
Molecclare, Istituto Giannina Gaslini, Largo G. Gaslini 5, Genova
16148, Italia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 26; Length 3410; Pred. No. 5.00e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 22; Length 7218
Pred. No. 5.00e-08;
61; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.

1 (bases)

Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.

Recombinant fowlpox virus

Patent: US 5670367-A 14 23 SEP-1997;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTACCGGTTCGGAATTCCCGGGTCGACCCACGCGTCCGGAAGGCT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="kidney inner medulla"
587. .2431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1929 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I66494 7218 bp DNA
Sequence 14 from patent US 5670367.
I66494
                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"B18"
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1486 9
                                                                                                                                                                                                                                                                                                         /chromosome="12"
                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                           /map="12p13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 7.7%;
Best Local Similarity 4.3%;
Matches 4; Conservative
                                                                                                                      (bases 1 to 3410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1491 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o 066
                                                                                                                                                                                                                            1. .3410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92724471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
FEATURES
                                           AUTHORS
TITLE
                                                                                        JOURNAL
MEDLINE
                            REFERENCE
                                                                                                                      REFERENCE
                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

윱

```
CRELALLEPEFILKASLYAROOLNVRNYANNILAIAAFLPACRPHLRRYFCAIVOLLY
DWIQVAELY OSLAEGDKNKLVPLPACLRTAMTDKFAQFDEYOLAKYNPRKHRAKRHFR
RPPRSPGMEPPFSHRCFPRY IGFLREEQRKFEKAGDTVSEKKNPPRFTLKKLVVUKLH I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HKPAQHVQALLGYRYPSNLQLFSRSRLPGPWDSSRAGKRWKLSRPTWERELS.R.P.
ASVWEELIBNGKLPPMAMLRNLCNLLRVGISSRHBEIJLQRLQHGKSVIHSRQIPPT
LNAHDAIDALEAQLRNQALPPSNITLMRRILTRRRRRFLCHLSRGVALS.
IPVLYEQLKREKLYHRARQMKYGBRULMYRQALETAVNLSWRHSLPELLPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKTAIKLQAOVQEFDENDGWSLNTFGKYLLSILAGQRVPVDRYILLGQSWDDGB-1N-N:
QUWDRANSKOLFVGTLLKRYQYLSDDNBVDYVLSGCTDAILKFTAFRGASB-1-PN-
GQWDK IFKIPPPPOKTGVQSLRPLEEDTPSPLAPVSQGGWRSTRLFTSKTFK-N-PN-
GLLKSVLPALQARAAPHRISLHGIDLRWGVTEEETRRNRQLEVCLGEVUNAG...

DLLLRSVLPALQARAAPHRISLHGIDLRWGVTEEETRRNRQLEVCLGEVUNAG...

DSSRYSSYDDAWRSDSPVSESERAACHISELKSYLSRQKGITCRRYPCDWGAACHIV
NGGLEEFGQLVLQDVWMMIQKLYLQPGALLEQPVSIPODDLVQATFQQLGKPPSIVAH
VGGLEEFGQLVLQDVWMMIQKLYLQPGALLEQPVSIPODDLVQATFQQLGKPPSIVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLLODTVOOLMLPHGRESLYTGOSGOGKTAFTASLVSALQAPDGAKVAPEVFFHFSGA
RPDQGLALTLLRRLCTYLRGOLKEPGALPSTYRSLVWELQQRLLPKSAESLHPGGTG
LIIDGADRLVDQNGQLISDMIPKKLPRCVHLVLSVSSDAGLGETLEGSGGAHVLAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQVSERLRTLPATVPLLLQHILSTLEKEHGPDVLPQALTALEVTRSGLTVDQLHGVI.»
VWRTLPRGTKSWEEAVAAGNSGDPYPMGPFACLVQSLRSLLGEGPLERPGARLCLPVC
PLRTAAKRCYGKRPGLEDTAHILIAAQLWKTCDADASGTFRSCPPEALGDLPYHLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DILSLENRCLATLPSLKSTVSASPLFQSLQISHMTQADLYRVNNSNCLLSEPPSWRAQ
HFSRGLDLSTCPIALKSISATETAQEATLGRWFDSEEKKGAETQMPSYSLSLGEEEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEASARARLVREELALYGKRLEESPFNNQMRLLLVKRESGRPLYLRLVTDHLRLFT!.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQQASILSQYPRLLPQQAANQPLDSPLCHQASLLSRRWHLQHTLRWLNKPRTMKNQCS
SSLSLAVSSSPTAVAFSTNGQRAAVGTANGTVYLLDLRTWQEEKSVVSGCDGISAC: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="telomerase-associated protein TP-1"
/db_xref="PID:g1848277"
/translation="MEKLHGHVSAHPDILSLENRCLAMLPDLQPLEKLHQHVSTHSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNRGLLSKFLTNLHVVAAHLELGLVSRLLEAHALYASSVPKEEQKLPEADVAVFRTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLATSQELLASASEDFTVQLWPRQLLTRPHKAEDFPCGTELRGHEGPVSCCSFSTDCG
SLATGGRDRSLLCWDVRTPKTPVLIHSFPACHRDWVTGCAWTKDNLLISCSSDGSVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLKNQCLATLPDLKTMEKPHGYVSAHPDILSLENQCLATLSDLKTMEKPHGHVSAHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLAVKLTSGDSESHPEPTDHVLQEKKMALLSLLCSTLVSEVNMNNTSDPTLAAIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSQGAQGQALDVAVSALAWLSPKVLVSGAEDGSLQGWALKECSLQSLWLLSRFQKPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 865)
Harrington,L., McPhall,T., Mar,V., Zhou,W., Oulton,R., Bass,M.B., Arruda,I. and Robinson,M.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robinson, M.O. and Harrington, L.
Direct Submission
Submitted (22-JAN-1997) Molecular Genetics, Amgen, Inc., 1840
Dehavilland Drive, Thousand Oaks, CA 91320, USA
Location/Qualifiers
149 tetttggtgetgetgegttgetaettttetggteaagaaagteaceaagaateeaetetett 90
                                                                                                                                                                                                                                                                                                                                         25-FEB-1997
                                                                                                                                                                                                                                                                            Human telomerase-associated protein TP-1 mRNA, complete cds. 91848276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A mammalian telomerase-associated protein
Science 275 (5302), 973-977 (1997)
                                                                              1405 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                      89 tececececttetgtegtetttegeageegtae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 8665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
```

```
/product="tazarotene-induced gene 2"
/db_xref="P1D:g1848264"
/db_xref="P1D:g1848264"
/db_xref="P1D:g1848264"
/dranslation="MRRLIPPALIPLALMLGAVGVGVAELTEAQRRGLQVALEEFHKHPPVQ
/Aranslation="MRRLIPPALIPREFILOGYSCRKRDWKRPECKVRPNGRKRKCLACI
KLGSEDKVLGRLVHCPIETQVLREAEEHQETGCLRVQRAGEDPHSFYPPGQFAFSKAL
WDPESGQRLGQFLGHQSAVSAVAAVEEHVVSVSRDGTLKVWDHQGVELTSIPAHSGPI
SHCAAAMEPRAAGPESELLVVTVGLDGATRLWHPLLVCQTHTLGHSGSPVRAAAVSE
TSGLMLTASEDGSVRLWQVPKEADDTCIPRSSAAVTAVAWAPDGSMAVSGNQACELIL
WQEARAVATAQAPGHIGALIWSSAHTFVLSADEKISEWQVKLRKGSAPGNLSLHLNR
ILQEDLGVLTSLDMAPDGHFLILLARADLKLLCMKPGDAPSETWSSYTENPMILSTHKE
YGIFVLQPKDPGVLSFLRQKESGEFEERLNFDINLENPSRTLISITQAKPESESSFLC
                                                                                                               ASSDGILMNLAKCSPEGEWTTGNMQKKANTPETQTPGTDPSTCRESDASMDSDASMD
SEPTPHLKTRQRRKIHSGSVTALHVLPELLVTASKDRDVKLWERPSMQLLGLFRCEGS
VSCLEPWLGANSTLQLAVGDVQGNVYFLNWE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 770)
Nagpat,S., Patel,S., Jacobs,H., DiSepio,D., Ghosn,C., Malhotra,M.,
Teng,M., Duvic,M. and Chandraratna,R.A.S.
Tazarotene-induced gene 2 (TIG2), a novel retinoid responsive gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon.9606"
/fb_xref="taxon.9606"
/fissue_type="retinoid (tazarotene) treated and untreated
/kin graft cultures of foreskin keratinocytes and dermal
fibroblasts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 770)
Nagpal,S., Patel,S. and Chandraratna,R.A.S.
Direct Submission
Submitted (06-NOV-1996) Biochemistry, Allergan Inc., 2525 Dupont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1997
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSU77594 770 bp mRNA PRI 25-FEB-1
Human tazarotene-induced gene 2 (TIG2) mRNA, complete cds
91848263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                      Length 8665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 770;
                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                        Score 36; DB 28; 1
Pred. No. 5.00e-08;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                     1 GGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 39
                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 27; 1
Pred. No. 4.85e-06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 36
                                                                                                                                                                                                                1946 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dr., Irvine, CA 92713, USA
Location/Qualifiers
1. .770
                                                                                                                                                                                                                2410 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                     8492. .8665
/rpt_family="ALU"
1 2360 c 2410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TIG2"
97. .588
                                                                                                                                                                                                                                                                      7.7%;
larity 94.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="TIG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%;
Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 37; Conser
                                                                                                                                                                                                                    ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in skin
                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
/ product = Perfly; 2PT3-1"
// product = Perfly; 2PT3-1"
// db_xref="PlD:dd101956"
// db_xref="PlD:dd101967"
// db_xref="P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seven zinc-finger transcription factors are expressed sequentially during the development of anthers and pollen in Petunia Unpublished (1997)

2 (bases 1 to 1640)

Takatsuji, H.

Direct Submission

Submitted (14-JAN-1997) to the DDBJ/EMBL/GenBank databases. Hiroshi Takatsuji, National Institute of Agrobiological Resources, Plant Physiology; 2-1-2 Kannondai, Tsukuba, Ibaraki 305, Japan (Tel:0298-38-888) Fax:0298-38-7417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ċ
                          AB000453 1640 bp mRNA PLN 28-JAN-1997
AB000453
AB000453
Zinc finger protein; ZPT3; transcription factor.
Zinc finger protein; ZPT3; transcription factor.
Zinc finger protein; ZPT3; transcription factor.
Detunia x hybrida (cultivar:Mitchell diploid, lab_host:Escherichia Petunia x hybrida
Eukaryotae; mitchohondrial eukaryotes; Viridiplantae; charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Magnollophyta; Magnollophyta; Solananae; Solanales; Solanales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Cys(2) His(2) zinc finger protein, 3 fingers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kobayashi, A., Sakamoto, A., Kubo, K., Rybka, Z., Kanno, Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="Escherichia coli, DH10B"
/tissue_type="stamen"
95. .1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 24; Le
Pred. No. 4.85e-06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Petunia x hybrida"
/cultivar="Mitchell diploid"
/db_xref="taxon:4102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: Mon Mar 8 21:44:01 1999 Job time: 1711 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="ZPT3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.1%;
Best Local Similarity 94.4%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takatsuji,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (sites)
    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```